BLAST Basic Local Alignment Search Tool

-

Protein sequence(220 letters)

Results for: lcl|11706 None(220aa) ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
    lcl|11706
Description
    None
Molecule type
    amino acid
Query Length
    220

Database Name
    nr
Description
    All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program
    BLASTP 2.2.18+ Citation

Reference
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Reference
Reference - compositional score matrix adjustment
Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Window Size	40

Database

Posted date	May 13, 2008 5:55 PM

Number of letters   2,229,583,460
Number of sequences 6,530,794
Entrez query   none

Karlin-Altschul statistics

Params	Gapped	Ungapped
Lambda	0.322234	0.267
K	0.13584	0.041
H	0.392855	0.14

Results Statistics

Length adjustment	129
Effective length of query	91
Effective length of database	1387111034
Effective search space	126227104094
Effective search space used	126227104094

Graphic Summary
Show Conserved Domains
Putative conserved domains have been detected, click on the image below for detailed results.


Distribution of 101 Blast Hits on the Query Sequence

?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.
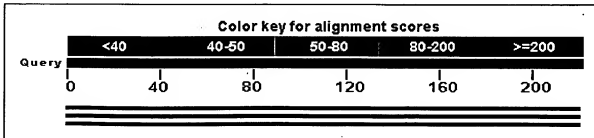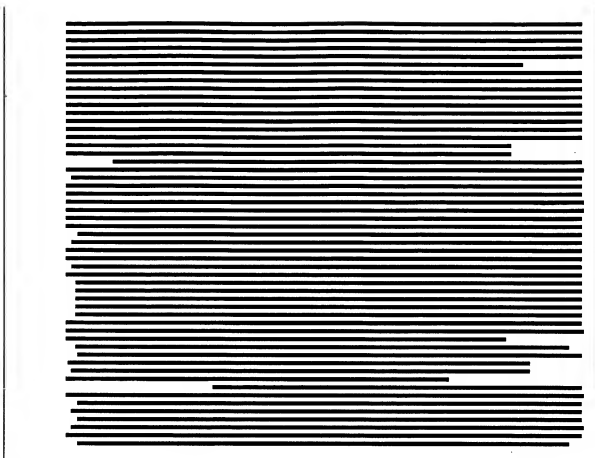
Descriptions
Legend for links to other resources: 🅄 UniGene 🅴 GEO 🅶 Gene 🆂 Structure 🅼 Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

ABK22119.1	unknown [Picea sitchensis] >gb|ABK25940.1| unknown [Picea sitchensis]	406	406	99%	4e-112	
NP_001059109.1	Os07g0194000 [Oryza sativa (japonica cultivar-group) >dbj|BAD30158.1| synaptobrevin-like protein [Oryza sativa Japonica Group) >emb|CAD70274.1| synaptobrevin 1 [Oryza sativa (japonica cultivar-group)] >dbj|BAF21023.1| Os07g0194000 [Oryza sativa (japonica cultivar-group)]	389	389	99%	9e-107	🅄🅶
NP_001051606.1	Os03g0803000 [Oryza sativa (japonica cultivar-group) >gb|AAO72389.1| synaptobrevin-like protein [Oryza sativa (japonica cultivar-group) >gb|ABF99408.1| Vesicle-associated membrane protein 724, putative, expressed [Oryza sativa (japonica cultivar-group)] >dbj|BAF13520.1| Os03g0803000 [Oryza sativa (japonica cultivar-group)]	387	387	99%	2e-106	🅄🅶
CAO68808.1	unnamed protein product [Vitis vinifera]	385	385	99%	8e-106	
CAO63820.1	unnamed protein product [Vitis vinifera]	385	385	99%	8e-106	
NP_171968.1	ATVAMP726 (VESICLE-ASSOCIATED MEMBRANE PROTEIN) [Arabidopsis thaliana] >sp|Q9MAS5|VA726_ARATH Putative vesicle-associated membrane protein 726 (AtVAMP726)	384	384	99%	2e-105	🅄🅶
CAN81365.1	hypothetical protein [Vitis vinifera] >emb|CAO41974.1| unnamed protein product [Vitis vinifera]	384	384	99%	2e-105	
NP_180826.2	ATVAMP725 (Arabidopsis thaliana vesicle-associated membrane protein 725) >sp|O48850|VA725_ARATH Vesicle-associated membrane protein 725 (AtVAMP725) >dbj|BAC42934.1| putative synaptobrevin [Arabidopsis thaliana] >gb|AAP06822.1| putative synaptobrevin protein [Arabidopsis thaliana]	379	379	99%	6e-104	🅄🅶
AAQ15287.1	synptobrevin-related protein [Pyrus pyrifolia]	379	379	88%	1e-103	
AAC04496.1	putative synaptobrevin [Arabidopsis thaliana]	378	378	99%	1e-103	
NP_171967.1	VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabidopsis thaliana] >sp|Q9ZTW3|VA721_ARATH Vesicle-associated membrane protein 721 (AtVAMP721) (v-SNARE synaptobrevin 7B) (AtVAMP7B) >gb|AAC98905.1| vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana] >gb|AAL85003.1| At1g04740/T1G11_1 [Arabidopsis thaliana] >gb|AAM91491.1| At1g04740/T1G11_1 [Arabidopsis thaliana] >dbj|BAD42978.1| putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj|BAD43361.1| putative vesicle-associated membrane protein, synaptobrevin 7B	378	378	99%	1e-103	🅄🅶

[Arabidopsis thaliana] >dbj|BAD43374.1|
putative vesicle-associated membrane protein,
synaptobrevin 7B [Arabidopsis thaliana]
>dbj|BAD43437.1| putative vesicle-associated
membrane protein, synaptobrevin 7B
[Arabidopsis thaliana] >dbj|BAD43557.1|
putative vesicle-associated membrane protein,
synaptobrevin 7B [Arabidopsis thaliana]
>dbj|BAD43592.1| putative vesicle-associated
membrane protein, synaptobrevin 7B
[Arabidopsis thaliana] >dbj|BAD43735.1|
putative vesicle-associated membrane protein,
synaptobrevin 7B [Arabidopsis thaliana]
>dbj|BAD43994.1| putative vesicle-associated
membrane protein, synaptobrevin 7B
[Arabidopsis thaliana] >dbj|BAD44048.1|
putative vesicle-associated membrane protein,
synaptobrevin 7B [Arabidopsis thaliana]
>dbj|BAD44054.1| putative vesicle-associated
membrane protein, synaptobrevin 7B
[Arabidopsis thaliana] >dbj|BAD44149.1|
putative vesicle-associated membrane protein,
synaptobrevin 7B [Arabidopsis thaliana]
>dbj|BAD44415.1| putative vesicle-associated
membrane protein, synaptobrevin 7B
[Arabidopsis thaliana] >dbj|BAD44419.1|
putative vesicle-associated membrane protein,
synaptobrevin 7B [Arabidopsis thaliana]
>dbj|BAD44642.1| putative vesicle-associated
membrane protein, synaptobrevin 7B
[Arabidopsis thaliana]

BAD43410.1	putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana]	377	377	99%	3e-103
AAF40460.1	Strong similarity to the synaptobrevin homolog F25I18.14 gi|2924792 from A. thaliana on BAC gb|AC002334. [Arabidopsis thaliana]	377	377	99%	3e-103
NP_180871.1	SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis thaliana] >sp|P47192|VA722_ARATH Vesicle-associated membrane protein 722 (AtVAMP722) (Synaptobrevin-related protein 1) >gb|AAL31896.1|AF419564_1 At2g33120/F25I18.14 [Arabidopsis thaliana] >gb|AAC04921.1| putative synaptobrevin [Arabidopsis thaliana] >gb|AAL62414.1| putative synaptobrevin [Arabidopsis thaliana] >gb|AAL79587.1| At2g33120/F25I18.14 [Arabidopsis thaliana] >gb|AAM48025.1| putative synaptobrevin [Arabidopsis thaliana] >gb|AAM64431.1| putative synaptobrevin [Arabidopsis thaliana] >gb|AAM91096.1| At2g33120/F25I18.14 [Arabidopsis thaliana]	369	369	99%	9e-101 U G
AAA56991.1	formerly called HAT24; synaptobrevin-related protein	365	365	99%	8e-100
NP_001031469.1	SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis thaliana]	360	360	99%	3e-98 U G
ABK92923.1	unknown [Populus trichocarpa] >gb|ABK94486.1| unknown [Populus trichocarpa] >gb|ABK95420.1| unknown [Populus trichocarpa]	357	357	99%	2e-97
EAZ03095.1	hypothetical protein OsI_024327 [Oryza sativa (indica cultivar-group)] >gb|EAZ39005.1| hypothetical protein OsJ_022488 [Oryza sativa (japonica cultivar-group)]	357	357	99%	4e-97

EAZ28954.1	hypothetical protein OsJ_012437 [Oryza sativa (japonica cultivar-group)]	351	351	85%	2e-95
EAY92225.1	hypothetical protein OsI_013458 [Oryza sativa (indica cultivar-group)]	351	351	85%	2e-95
CAN65946.1	hypothetical protein [Vitis vinifera]	349	349	90%	6e-95
ABK24294.1	unknown [Picea sitchensis]	349	349	100%	9e-95
NP_001049070.1	Os03g0165800 [Oryza sativa (japonica cultivar-group)] >gb|ABF94152.1| Vesicle-associated membrane protein 724, putative, expressed [Oryza sativa (japonica cultivar-group)] >dbj|BAF10984.1| Os03g0165800 [Oryza sativa (japonica cultivar-group)] >gb|EAY88679.1| hypothetical protein OsI_009912 [Oryza sativa (indica cultivar-group)]	346	346	98%	7e-94 U G
XP_001777330.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb|EDQ57860.1| R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	326	326	99%	8e-88 U G
CAO70980.1	unnamed protein product [Vitis vinifera]	325	325	99%	1e-87
ABK27118.1	unknown [Picea sitchensis]	325	325	100%	2e-87
ABK23325.1	unknown [Picea sitchensis]	319	319	100%	6e-86
O23429	Vesicle-associated membrane protein 724 (AtVAMP724) (SYBL1-like protein) >gb|AAT41760.1| At4g15780 [Arabidopsis thaliana] >gb|AAT70463.1| At4g15780 [Arabidopsis thaliana]	318	318	99%	2e-85
XP_001784148.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb|EDQ51072.1| R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	317	317	99%	3e-85 U G
AAV49990.1	putative synaptobrevin/VAMP [Hordeum vulgare subsp. vulgare]	303	303	97%	5e-81
ABK95406.1	unknown [Populus trichocarpa]	293	293	98%	4e-78
NP_190998.1	ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane protein 727) >ref|NP_001078283.1| ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane protein 727) >sp|Q9M376|VA727_ARATH Vesicle-associated membrane protein 727 (AtVAMP727) >emb|CAB71004.1| synaptobrevin-like protein [Arabidopsis thaliana] >gb|AAS47612.1| At3g54300 [Arabidopsis thaliana] >gb|AAS76729.1| At3g54300 [Arabidopsis thaliana] >dbj|BAF00993.1| synaptobrevin - like protein [Arabidopsis thaliana]	293	293	99%	4e-78 G
NP_850201.1	ATVAMP723 (Arabidopsis thaliana vesicle-associated membrane protein 723) >sp|Q8VY69|VA723_ARATH Vesicle-associated membrane protein 723 (AtVAMP723) >gb|AAL62392.1| putative synaptobrevin [Arabidopsis thaliana] >gb|AAN15528.1| putative synaptobrevin [Arabidopsis thaliana]	289	289	98%	1e-76 U G
NP_001062495.1	Os08g0558600 [Oryza sativa (japonica cultivar-group)] >dbj|BAD13129.1| putative	286	286	98%	7e-76 U G

vesicle-associated membrane protein 725
(AtVAMP725) [Oryza sativa Japonica Group]
>dbj|BAF24409.1| Os08g0558600 [Oryza sativa
(japonica cultivar-group)]

CAO63919.1	unnamed protein product [Vitis vinifera]	285	285	99%	2e-75
CAJ15414.1	unnamed protein product [Triticum aestivum]	283	283	97%	5e-75
CAJ13968.1	unnamed protein product [Aegilops tauschii]	283	283	97%	7e-75
CAJ13552.1	unnamed protein product [Triticum turgidum]	283	283	97%	8e-75
CAJ13539.1	unnamed protein product [Triticum aestivum]	282	282	97%	1e-74
AAS88558.1	putative synaptobrevin [Triticum monococcum]	281	281	97%	2e-74
NP_001030968.1	VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabidopsis thaliana] >dbj|BAD44122.1| putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana]	280	280	99%	6e-74 **UG**
XP_001779971.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb|EDQ55180.1| R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	278	278	100%	2e-73 **G**
NP_193313.2	ATVAMP724 (Arabidopsis thaliana vesicle-associated membrane protein 724)	275	275	85%	2e-72 **UG**
XP_001692216.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb|EDP04166.1| R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	268	268	95%	2e-70 **UG**
NP_001059291.1	Os07g0249200 [Oryza sativa (japonica cultivar-group)] >dbj|BAC20811.1| putative Vesicle-associated membrane protein [Oryza sativa Japonica Group] >dbj|BAD30660.1| putative Vesicle-associated membrane protein [Oryza sativa Japonica Group] >dbj|BAF21205.1| Os07g0249200 [Oryza sativa (japonica cultivar-group)]	266	266	97%	9e-70 **UG**
EAZ07996.1	hypothetical protein OsI_029228 [Oryza sativa (indica cultivar-group)]	263	263	89%	5e-69
EAZ43645.1	hypothetical protein OsJ_027128 [Oryza sativa (japonica cultivar-group)]	263	263	88%	7e-69
AAC04922.1	putative synaptobrevin [Arabidopsis thaliana]	261	261	74%	2e-68
AAB80624.1	Strong similarity to Arabidopsis ATHSAR1 (gb|M90418). ESTs gb|T44122,gb|N65276,gb|AA041135 come from this gene. [Arabidopsis thaliana]	260	260	71%	4e-68
XP_001764415.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb|EDQ70682.1| R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	260	260	100%	5e-68 **G**
EAZ39281.1	hypothetical protein OsJ_022764 [Oryza sativa (japonica cultivar-group)]	253	253	97%	6e-66
EAZ25708.1	hypothetical protein OsJ_009191 [Oryza sativa (japonica cultivar-group)]	252	252	98%	1e-65
XP_001418265.1	predicted protein [Ostreococcus lucimarinus CCE9901] >gb|ABO96558.1| predicted protein [Ostreococcus lucimarinus CCE9901]	246	246	97%	6e-64 **G**
XP_001777794.1		244	244	99%	4e- **G**

	Description				
	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb|EDQ57456.1| R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]			63	
NP_001067392.1	Os12g0639800 [Oryza sativa (japonica cultivar-group)] >gb|ABA99617.1| Synaptobrevin family protein, expressed [Oryza sativa (japonica cultivar-group)] >dbj|BAF30411.1| Os12g0639800 [Oryza sativa (japonica cultivar-group)]	236	236	99%	9e-61	U G
XP_001692208.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb|EDP04158.1| R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	217	217	95%	6e-55	U G
EAZ03380.1	hypothetical protein OsI_024612 [Oryza sativa (indica cultivar-group)]	201	272	97%	3e-50	
XP_001692312.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb|EDP04262.1| R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	186	186	95%	9e-46	U G
CAL53602.1	SYNAPTOBREVIN-RELATED PROTEIN 1 (IC) [Ostreococcus tauri]	182	182	83%	1e-44	
XP_001692324.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb|EDP04274.1| R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	182	182	90%	1e-44	U G
NP_196676.1	ATVAMP713 (Arabidopsis thaliana vesicle-associated membrane protein 713) >sp|Q9LFP1|VA713_ARATH Vesicle-associated membrane protein 713 (AtVAMP713) >emb|CAB96650.1| putative protein [Arabidopsis thaliana] >gb|AAM14024.1| unknown protein [Arabidopsis thaliana] >gb|AAM67467.1| unknown protein [Arabidopsis thaliana]	167	167	96%	4e-40	U G
NP_197628.1	ATVAMP714 (Vesicle-associated membrane protein 714) [Arabidopsis thaliana] >sp|Q9FMR5|VA714_ARATH Vesicle-associated membrane protein 714 (AtVAMP714) >dbj|BAB08335.1| synaptobrevin-like protein [Arabidopsis thaliana]	161	161	96%	2e-38	U G
ABM30199.2	synaptobrevin-like protein [Brassica juncea]	161	161	96%	3e-38	
B71423	hypothetical protein - Arabidopsis thaliana >emb|CAB10356.1| SYBL1 like protein [Arabidopsis thaliana] >emb|CAB78620.1| SYBL1 like protein [Arabidopsis thaliana]	160	160	50%	5e-38	
NP_194942.1	VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C) [Arabidopsis thaliana] >sp|O49377|VA711_ARATH Vesicle-associated membrane protein 711 (AtVAMP711) (v-SNARE synaptobrevin 7C) (AtVAMP7C) >gb|AAL27509.1|AF439840_1 AT4g32150/F10N7_40 [Arabidopsis thaliana] >emb|CAA16574.1| synaptobrevin-like protein [Arabidopsis thaliana] >gb|AAD01748.1| vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana] >emb|CAB79933.1| synaptobrevin-like protein [Arabidopsis thaliana] >gb|AAM65673.1| synaptobrevin-like protein [Arabidopsis thaliana] >gb|AAM78063.1| AT4g32150/F10N7_40 [Arabidopsis thaliana] >dbj|BAE98551.1| vesicle-associated membrane protein 7C	156	156	96%	1e-36	U G

[Arabidopsis thaliana]

CAO44255.1	unnamed protein product [Vitis vinifera]	156	156	96%	1e-36	
XP_001762112.1	R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens] >gb|EDQ73216.1| R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]	156	156	86%	1e-36	U G
NP_001064184.1	Os10g0154000 [Oryza sativa (japonica cultivar-group) >gb|ABB46773.2| Synaptobrevin family protein, expressed [Oryza sativa (japonica cultivar-group)] >dbj|BAF26098.1| Os10g0154000 [Oryza sativa (japonica cultivar-group)]	156	156	97%	1e-36	U G
XP_001778044.1	R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens] >gb|EDQ57153.1| R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]	155	155	86%	2e-36	U G
XP_001631076.1	predicted protein [Nematostella vectensis] >gb|EDO39013.1| predicted protein [Nematostella vectensis]	155	155	96%	2e-36	G
XP_001769494.1	R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens] >gb|EDQ65655.1| R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]	154	154	86%	5e-36	U G
ABK93000.1	unknown [Populus trichocarpa]	150	150	96%	4e-35	
XP_001698008.1	R-SNARE protein, VAMP71-family [Chlamydomonas reinhardtii] >gb|EDO99593.1| R-SNARE protein, VAMP71-family [Chlamydomonas reinhardtii]	150	150	97%	6e-35	U G
XP_001745842.1	predicted protein [Monosiga brevicollis MX1] >gb|EDQ89266.1| predicted protein [Monosiga brevicollis MX1]	149	149	88%	1e-34	G
XP_001879548.1	VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H82] >gb|EDR10163.1| VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H82]	148	148	94%	3e-34	G
EAY77730.1	hypothetical protein OsI_031689 [Oryza sativa (indica cultivar-group)]	146	146	97%	9e-34	
AAM14694.1	Putative synaptobrevin-like protein [Oryza sativa (japonica cultivar-group)] >gb|EAZ15333.1| hypothetical protein OsJ_029542 [Oryza sativa (japonica cultivar-group)]	146	146	97%	9e-34	
XP_642704.1	synaptobrevin domain-containing protein [Dictyostelium discoideum AX4] >sp|Q86AQ7.1|VAM7B_DICDI Vesicle-associated membrane protein 7B >gb|AAO51196.1| similar to Arabidopsis thaliana (Mouse-ear cress). Synaptobrevin-like protein [Dictyostelium discoideum] >gb|EAL68772.1| synaptobrevin domain-containing protein [Dictyostelium discoideum AX4]	146	146	96%	1e-33	U G
NP_001056946.1	Os06g0174400 [Oryza sativa (japonica cultivar-group)] >dbj|BAA95814.1| putative synaptobrevin 1 [Oryza sativa Japonica Group] >dbj|BAF18860.1| Os06g0174400 [Oryza sativa (japonica cultivar-group)]	145	145	96%	1e-33	U G
ABK95432.1	unknown [Populus trichocarpa]	145	145	96%	2e-33	

XP_001635801.1	predicted protein [Nematostella vectensis] >gb|EDO43738.1| predicted protein [Nematostella vectensis]	140	140	85%	5e-32 G
NP_180106.1	ATVAMP712 (Arabidopsis thaliana vesicle-associated membrane protein 712) >sp|Q9SIQ9|VA712_ARATH Vesicle-associated membrane protein 712 (AtVAMP712) >gb|AAD23657.1| putative synaptobrevin [Arabidopsis thaliana]	140	140	96%	5e-32 UG
NP_001048427.1	Os02g0803600 [Oryza sativa (japonica cultivar-group)] >dbj|BAD36041.1| putative synaptobrevin 1 [Oryza sativa Japonica Group] >dbj|BAF10341.1| Os02g0803600 [Oryza sativa (japonica cultivar-group)]	137	137	95%	4e-31 UG
NP_001086871.1	synaptobrevin-like 1 [Xenopus laevis] >gb|AAH77586.1| Sybl1-prov protein [Xenopus laevis]	137	137	86%	5e-31 UG
XP_566592.1	vesicle-associated membrane protein 712 [Cryptococcus neoformans var. neoformans JEC21] >gb|AAW40773.1| vesicle-associated membrane protein 712, putative [Cryptococcus neoformans var. neoformans JEC21]	136	136	86%	8e-31 G
XP_778199.1	hypothetical protein CNBA1990 [Cryptococcus neoformans var. neoformans B-3501A] >gb|EAL23552.1| hypothetical protein CNBA1990 [Cryptococcus neoformans var. neoformans B-3501A]	136	136	86%	1e-30 G
NP_001026292.1	synaptobrevin-like 1 [Gallus gallus] >sp|Q5ZL74.1|VAMP7_CHICK Vesicle-associated membrane protein 7 (Synaptobrevin-like protein 1) >emb|CAG31519.1| hypothetical protein [Gallus gallus]	135	135	86%	1e-30 UG
ABP03854.1	Longin-like [Medicago truncatula]	135	135	95%	2e-30
NP_610524.1	CG1599 CG1599-PA [Drosophila melanogaster] >gb|AAF58892.1| CG1599-PA [Drosophila melanogaster] >gb|AAL49317.1| RH15778p [Drosophila melanogaster]	135	135	95%	2e-30 UG
NP_035645.1	vesicle-associated membrane protein 7 [Mus musculus] >sp|P70280.1|VAMP7_MOUSE Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) >emb|CAA65509.1| synaptobrevin-like protein [Mus musculus] >emb|CAB94231.1| synaptobrevin-like protein [Mus musculus] >dbj|BAB22386.1| unnamed protein product [Mus musculus] >dbj|BAB27667.1| unnamed protein product [Mus musculus] >gb|AAH03764.1| Synaptobrevin like 1 [Mus musculus] >dbj|BAC40712.1| unnamed protein product [Mus musculus] >dbj|BAE38126.1| unnamed protein product [Mus musculus] >gb|ABK42476.1| VAMP7 [synthetic construct] >gb|EDL07809.1| synaptobrevin like 1, isoform CRA_c [Mus musculus]	134	134	86%	4e-30 UG
CAH69613.1	synaptobrevin 1-2 [Paramecium tetraurelia]	134	134	97%	4e-30
XP_001439963.1	hypothetical protein GSPATT00008957001 [Paramecium tetraurelia strain d4-2] >emb|CAD97455.1| synaptobrevin 1 [Paramecium tetraurelia] >emb|CAK72566.1| unnamed protein	134	134	97%	4e-30 G

	product [Paramecium tetraurelia]				
XP_795809.2	PREDICTED: similar to Sybl1-prov protein [Strongylocentrotus purpuratus] >ref|XP_001188931.1| PREDICTED: similar to Sybl1-prov protein [Strongylocentrotus purpuratus]	134	134	96%	5e-30 **U G**
BAD96514.1	synaptobrevin-like 1 variant [Homo sapiens]	134	134	96%	6e-30 **G**
NP_005629.1	vesicle-associated membrane protein 7 [Homo sapiens] >ref|XP_001100334.1| PREDICTED: synaptobrevin-like 1 isoform 3 [Macaca mulatta] >ref|XP_001498248.1| PREDICTED: similar to ORF isoform 1 [Equus caballus] >sp|P51809.3|VAMP7_HUMAN Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) (Tetanus-insensitive VAMP) (Ti-VAMP) >emb|CAA63133.1| ORF [Homo sapiens] >emb|CAB96816.1| synaptobrevin-like 1 protein [Homo sapiens] >gb|AAH56141.1| Vesicle-associated membrane protein 7 [Homo sapiens] >gb|EAW55882.1| synaptobrevin-like 1, isoform CRA_e [Homo sapiens] >gb|EAW55883.1| synaptobrevin-like 1, isoform CRA_e [Homo sapiens]	133	133	96%	8e-30 **U G**
XP_855489.1	PREDICTED: similar to Synaptobrevin-like protein 1 [Canis familiaris]	133	133	96%	9e-30 **U G**
XP_001459953.1	hypothetical protein GSPATT00025290001 [Paramecium tetraurelia strain d4-2] >emb|CAK92556.1| unnamed protein product [Paramecium tetraurelia]	133	133	97%	9e-30 **U G**
NP_445983.1	vesicle-associated membrane protein 7 [Rattus norvegicus] >sp|Q9JHW5.1|VAMP7_RAT Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) >gb|AAF88059.1|AF281632_1 vesicle-associated membrane protein 7 [Rattus norvegicus] >gb|EDL43883.1| synaptobrevin-like 1, isoform CRA_b [Rattus norvegicus]	133	133	96%	9e-30 **U G**
NP_001069770.1	vesicle-associated membrane protein 7 [Bos taurus] >sp|Q17QI5.1|VAMP7_BOVIN Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) >gb|AAI18342.1| Similar to Synaptobrevin-like protein 1 [Bos taurus]	133	133	96%	9e-30 **U G**
BAE99604.1	synaptobrevin-like protein [Arabidopsis thaliana]	133	133	79%	1e-29

Alignments Select All Get selected sequences Distance tree of results

```
>gb|ABK22119.1|  unknown [Picea sitchensis]
 gb|ABK25940.1|  unknown [Picea sitchensis]
Length=222

 Score =  406 bits (1044),  Expect = 4e-112, Method: Compositional matrix adjust.
 Identities = 187/219 (85%),  Positives = 206/219 (94%),  Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE  60
            MGQQSLIY+FVARGTV+LAEYTEF GNFTTIA+QCL KLPASNNKFTYNCD HTFNYLVE
Sbjct  1    MGQQSLIYSFVARGTVVLAEYTEFKGNFTTIAAQCLQKLPASNNKFTYNCDNHTFNYLVE  60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGF YCVVA ESVG+Q+P+AF++RVKEDF +RYGGG+A TA  NSLNR+FGSKLKEHMQY
Sbjct  61   DGFAYCVVADESVGRQVPMAFLERVKEDFKRRYGGGRADTAVGNSLNRDFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLR QAQDF++QG
Sbjct  121  CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRFQAQDFKQQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T +RRKMW QNMK+KLIVLGI++ALILII+LSVCHGF C
Sbjct  181  TQLRRKMWFQNMKVKLIVLGIVVALILIIVLSVCHGFNC  219


>ref|NP_001059109.1|  U G Os07g0194000 [Oryza sativa (japonica cultivar-group)]
 dbj|BAD30158.1|  G synaptobrevin-like protein [Oryza sativa Japonica Group]
 emb|CAD70274.1|  G synaptobrevin 1 [Oryza sativa (japonica cultivar-group)]
 dbj|BAF21023.1|  G Os07g0194000 [Oryza sativa (japonica cultivar-group)]
Length=220

 GENE ID: 4342638 Os07g0194000 | Os07g0194000 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score =  389 bits (999),  Expect = 9e-107, Method: Compositional matrix adjust.
 Identities = 212/219 (96%),  Positives = 217/219 (99%),  Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE  60
            MGQQSLIYAFVARGTV+LAEYTEFTGNFTTIA+QCL KLPASNNKFTYNCDGHTFNYLVE
Sbjct  1    MGQQSLIYAFVARGTVVLAEYTEFTGNFTTIAAQCLQKLPASNNKFTYNCDGHTFNYLVE  60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGFTYCVVAVESVG+QIPIAF+DRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY
Sbjct  61   DGFTYCVVAVESVGRQIPIAFLDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG
Sbjct  121  CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC
Sbjct  181  TKVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219


>ref|NP_001051606.1|  U G Os03g0803000 [Oryza sativa (japonica cultivar-group)]
 gb|AAO72389.1|  G synaptobrevin-like protein [Oryza sativa (japonica cultivar-gr
 gb|ABF99408.1|  G Vesicle-associated membrane protein 724, putative, expressed
[Oryza sativa (japonica cultivar-group)]
 dbj|BAF13520.1|  G Os03g0803000 [Oryza sativa (japonica cultivar-group)]
Length=220

 GENE ID: 4334472 Os03g0803000 | Os03g0803000 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)
```

```
Score = 387 bits (995),  Expect = 2e-106, Method: Compositional matrix adjust.
Identities = 211/219 (96%), Positives = 216/219 (98%), Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE
Sbjct  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60

Query  61   DGFTYCVVAVESVGGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGFTYCVVAVESVG+QIPIAF+DRVK+DFTKRY GGKAATAAANSLNR+FGSKLKEHMQY
Sbjct  61   DGFTYCVVAVESVGRQIPIAFLDRVKDDFTKRYAGGKAATAAANSLNRDFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQ G
Sbjct  121  CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQAG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC
Sbjct  181  TQVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
```

>emb|CAO68808.1| unnamed protein product [Vitis vinifera]
Length=220

```
Score = 385 bits (990),  Expect = 8e-106, Method: Compositional matrix adjust.
Identities = 197/219 (89%), Positives = 212/219 (96%), Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            +GQQSLIY+FVARGTVILAEYTEFTGNFT+IA+QCL KLPASNNKFTYNCDGHTFNYLVE
Sbjct  2    VGQQSLIYSFVARGTVILAEYTEFTGNFTSIAAQCLQKLPASNNKFTYNCDGHTFNYLVE   61

Query  61   DGFTYCVVAVESVGGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVVAVES G+QIPIAF+RVK+DF KRYGGGKAATAVANGLNKEFGPKLKEHMQY
Sbjct  62   NGFTYCVVAVESAGRQIPIAFLERVKDDFNKRYGGGKAATAVANGLNKEFGPKLKEHMQY  121

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG
Sbjct  122  CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  181

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T +RRKMW+QNMKIKLIVLGIIIALILI+LS+CHGFKC
Sbjct  182  TKMRRKMWMQNMKIKLIVLGIIIALILIIVLSICHGFKC  220
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>emb|CAO63820.1| unnamed protein product [Vitis vinifera]
Length=219

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Score = 385 bits (990),  Expect = 8e-106, Method: Compositional matrix adjust.
Identities = 195/219 (89%), Positives = 212/219 (96%), Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGQQSLIY+FVARGTVILAE+TEF+GNFT+IA+QCL KLPA+NNKFTYNCDGHTFNYLVE
Sbjct  1    MGQQSLYSFVARGTVILAEFTEFSGNFTSIAAQCLQKLPATNNKFTYNCDGHTFNYLVE   60

Query  61   DGFTYCVVAVESVGGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DG+TYCVVAVE+VG+QIPIAF++RVKEDFTKRYGGGKAATA ANSLN+EFG KLKE MQY
Sbjct  61   DGYTYCVVAVEAVGRQIPIAFLERVKEDFTKRYGGGKAATAVANSLNKEFGPKLKEQMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG
Sbjct  121  CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T +RRKMWLQNMKIKLIVLGI+ALILII+LS+C GF C
Sbjct  181  TKMRRKMWLQNMKIKLIVLGILIALILIIVLSICGGFNC  219
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>ref|NP_171968.1| **UG** ATVAMP726 (VESICLE-ASSOCIATED MEMBRANE PROTEIN) [Arabidops
thaliana]
  sp|Q9MAS5|VA726_ARATH **G** Putative vesicle-associated membrane protein 726 (AtVAM
Length=220

  GENE ID: 839424 ATVAMP726 | ATVAMP726 (VESICLE-ASSOCIATED MEMBRANE PROTEIN)
[Arabidopsis thaliana] (10 or fewer PubMed links)

```
    Score = 384 bits (987),  Expect = 2e-105, Method: Compositional matrix adjust.
    Identities = 185/219 (84%), Positives = 207/219 (94%), Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGQQSLIY+FVARGTVILAEYTEF GNFT++A+QCL KLP+SNNKFTYNCDGHTFNYL +
Sbjct  1    MGQQSLIYSFVARGTVILAEYTEFKGNFTSVAAQCLQKLPSSNNKFTYNCDGHTFNYLAD   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVV +ES G+QIP+AF++RVKEDF KRYGGGKA+TA ANSLN+EFGSKLKEHMQY
Sbjct  61   NGFTYCVVVIESAGRQIPMAFLERVKEDFNKRYGGGKASTAKANSLNKEFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C DHPEE+SKL+KVKAQV+EVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR QG
Sbjct  121  CADHPEEISKLSKVKAQVTEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC                      219
            T ++RK+W +NMKIKLIV GII+ALILIIILSVCHGFKC
Sbjct  181  TKMKRKLWFENMKIKLIVFGIIVALILIIILSVCHGFKC                      219
```

>emb|CAN81365.1| hypothetical protein [Vitis vinifera]
 emb|CAO41974.1| unnamed protein product [Vitis vinifera]
Length=221

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    Score = 384 bits (986),  Expect = 2e-105, Method: Compositional matrix adjust.
    Identities = 176/219 (80%), Positives = 200/219 (91%), Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGQ+SLIYAFVARGTVILAEYTEF+GNF +IA QCL KLPA++NKFTYNCD HTF YL++
Sbjct  1    MGQKSLIYAFVARGTVILAEYTEFSGNFNSIAFQCLQKLPATSNKFTYNCDAHTFTYLLD   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +G+TYCVVA ESVG+Q+P+AF++R+++R+++DF  RYGG KAATA ANSLN++F SKLKEHMQY
Sbjct  61   NGYTYCVVAESVGRQVPMAFLERIRDDFVARYGGEKAATAPANSLNKDFSSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHPEE+SKLAKVK QV+EVKGVMMENIEKVLDRGEKIELLVDKT NL  QAQDFR  G
Sbjct  121  CVDHPEEISKLAKVKDQVSEVKGVMMENIEKVLDRGEKIELLVDKTHNLHEQAQDFRSAG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC                      219
            T +RRKMWLQNMKIKLIVLGI++ALILII+LSVCHGF C
Sbjct  181  TKIRRKMWLQNMKIKLIVLGILVALILIIVLSVCHGFNC                      219
```

>ref|NP_180826.2| **UG** ATVAMP725 (Arabidopsis thaliana vesicle-associated membran
725)
 sp|O48850|VA725_ARATH **G** Vesicle-associated membrane protein 725 (AtVAMP725)
 dbj|BAC42934.1| **G** putative synaptobrevin [Arabidopsis thaliana]
 gb|AAP06822.1| **G** putative synaptobrevin protein [Arabidopsis thaliana]
Length=285

GENE ID: 817827 ATVAMP725 | ATVAMP725 (Arabidopsis thaliana vesicle-associated
membrane protein 725) [Arabidopsis thaliana] (10 or fewer PubMed links)

```
    Score = 379 bits (974),  Expect = 6e-104, Method: Compositional matrix adjust.
    Identities = 192/219 (87%), Positives = 207/219 (94%), Gaps = 0/219 (0%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGQQ+LIY+FVARGTVIL EYTEF GNFT +A+QCL KLP+SNNKFTYNCDGHTFNYLVE
Sbjct  66   MGQQNLIYSFVARGTVILVEYTEFKGNFTAVAAQCLQKLPSSNNKFTYNCDGHTFNYLVE  125

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVVAVESVG+QIP+AF++RVKEDF KRYGGGKA TA ANSLNREFGSKLKEHMQY
Sbjct  126  NGFTYCVVAVESVGRQIPMAFLERVKEDFNKRYGGGKATTAQANSLNREFGSKLKEHMQY  185

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHP+E+SKLAKVKAQV+EVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR QG
Sbjct  186  CVDHPDEISKLAKVKAQVTEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTQG  245

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC                      219
            T +RRKMW +NMKIKLIVLGIII LILIIILSVC GFKC
Sbjct  246  TKIRRKMWFENMKIKLIVLGIIITLILIIILSVCGGFKC                      284
```

```
>gb|AAQ15287.1| synptobrevin-related protein [Pyrus pyrifolia]
Length=194

 Score = 379 bits (972), Expect = 1e-103, Method: Compositional matrix adjust.
 Identities = 174/194 (89%), Positives = 190/194 (97%), Gaps = 0/194 (0%)

Query  1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGGQSLIY+FVARGTVILAEYTEFTGNFT+IASQCL KLPLPA+NNKFTYNCDGHTFNYLV+
Sbjct  1    MGGQSLIYSFVARGTVILAEYTEFTGNFTSIASQCLQKLPATNNKFTYNCDGHTFNYLVD   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVVAVE+VG+Q+PIAF++R+KEDFT KRYGGGKAATA ANSLN+EFGSKLKEHMQY
Sbjct  61   NGFTYCVVAVEAVGRQVPIAFLERIKEDFTGRYGGGKAATAVANSLNREFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHPEE+SKL+KVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG
Sbjct  121  CVDHPEEISKLSKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180

Query  181  TNVRRKMWLQNMKI   194
            T +RRKMWLQNMK+
Sbjct  181  TQMRRKMWLQNMKL   194


>gb|AAC04496.1| putative synaptobrevin [Arabidopsis thaliana]
Length=220

 Score = 378 bits (971), Expect = 1e-103, Method: Compositional matrix adjust.
 Identities = 192/219 (87%), Positives = 207/219 (94%), Gaps = 0/219 (0%)

Query  1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGGQ+LIY+FVARGTVIL EYTEF GNFTAVAAQCLQKLPSSNNKFTYNCDGHTFNYLVE
Sbjct  1    MGGQNLIYSFVARGTVILVEYTEFKGNFTAVAAQCLQKLPSSNNKFTYNCDGHTFNYLVE   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVVAVESVG+QIP+AF++RVKEDF KRYGGGKA TA ANSLNREFGSKLKEHMQY
Sbjct  61   NGFTYCVVAVESVGRQIPMAFLERVKEDFNKRYGGGKATTAQANSLNREFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHP+E+SKLAKVKAQV+EVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR QG
Sbjct  121  CVDHPDEISKLSKVKAQVTEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILILIILSVCHGFKC   219
            T +RRKMW +NMKIKLIVLGIII LILIILSVC GFKC
Sbjct  181  TKIRRKMWFENMKIKLIVLGIIITLILIILSVCGGFKC   219


>ref|NP_171967.1| [U][G] VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabidops
thaliana]
    sp|Q9ZTW3|VA721_ARATH [G] Vesicle-associated membrane protein 721 (AtVAMP721) (v-
synaptobrevin 7B) (AtVAMP7B)
    gb|AAC98905.1| [G] vesicle-associated membrane protein 7B; synaptobrevin 7B [Arab
thaliana]
    16 more sequence titles

gb|AAL85003.1| [G] At1g04740/T1G11_1 [Arabidopsis thaliana]
    gb|AAM91491.1| [G] At1g04740/T1G11_1 [Arabidopsis thaliana]
    dbj|BAD42978.1| [G] putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
    dbj|BAD43361.1| [G] putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
    dbj|BAD43374.1| [G] putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
    dbj|BAD43437.1| [G] putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
    dbj|BAD43557.1| [G] putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
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dbj|BAD43592.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD43735.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD43994.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD44048.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD44054.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD44149.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD44415.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD44419.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
dbj|BAD44642.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
Length=219

GENE ID: 839419 VAMP7B | VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B)
[Arabidopsis thaliana] (10 or fewer PubMed links)

 Score = 378 bits (971), Expect = 1e-103, Method: Compositional matrix adjust.
 Identities = 190/219 (86%), Positives = 208/219 (94%), Gaps = 0/219 (0%)

```
Query    1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNCDGHTFNYLVE
Sbjct    1  MAQQSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNCDGHTFNYLVE   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGFTYCVVAV+S G+QIP++F++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY
Sbjct   61  DGFTYCVVAVDSAGRQIPMSFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+DHP+E+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR  G
Sbjct  121  CMDHPDEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTTG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T +RRKMWLQNMKIKLIVL IIIALILII+LSVCHGFKC
Sbjct  181  TQMRRKMWLQNMKIKLIVLAIIIALILIIIVLSVCHGFKC  219
```

>dbj|BAD43410.1| putative vesicle-associated membrane protein, synaptobrevin 7B
[Arabidopsis thaliana]
Length=219

 Score = 377 bits (969), Expect = 3e-103, Method: Compositional matrix adjust.
 Identities = 189/219 (86%), Positives = 208/219 (94%), Gaps = 0/219 (0%)

```
Query    1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNCDGHTFNYLVE
Sbjct    1  MAQQSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNCDGHTFNYLVE   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGFTYCVVAV+S G+QIP++F++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY
Sbjct   61  DGFTYCVVAVDSAGRQIPMSFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+DHP+E+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR  G
Sbjct  121  CMDHPDEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTTG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            + +RRKMWLQNMKIKLIVL IIIALILII+LSVCHGFKC
Sbjct  181  SQMRRKMWLQNMKIKLIVLAIIIALILIIIVLSVCHGFKC  219
```

>gb|AAF40460.1|AC004809_18 Strong similarity to the synaptobrevin homolog F25I18
from A. thaliana on BAC gb|AC002334. [Arabidopsis thaliana]

Length=229

```
 Score =  377 bits (967),  Expect = 3e-103, Method: Compositional matrix adjust.
 Identities = 185/228 (81%), Positives = 207/228 (90%), Gaps = 9/228 (3%)

Query  1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MGGQSLIY+FVARGTVILAEYTEF GNFT++A+QCL KLP+SNNKFTYNCDGHTFNYL +
Sbjct  1    MGGQSLIYSFVARGTVILAEYTEFKGNFTSVAAQCLQKLPSSNNKFTYNCDGHTFNYLAD   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVV +ES G+QIP+AF++RVKEDF KRYGGGKA+TA ANSLN+EFGSKLKEHMQY
Sbjct  61   NGFTYCVVVIESAGRQIPMAFLERVKEDFNKRYGGGKASTAKANSLNKEFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQ--------  172
            C DHPEE+SKL+KVKAQV+EVKGVMMENIEKVLDRGEKIELLVDKTENLRSQ
Sbjct  121  CADHPEEISKLSKVKAQVTEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQVNNNHISN  180

Query  173  -AQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
             AQDFR QGT ++RK+W +NMKIKLIV GII+ALILIIILSVCHGFKC
Sbjct  181  TAQDFRTQGTKMKRKLWFENMKIKLIVFGIIVALILIIILSVCHGFKC  228
```

>ref|NP_180871.1| UG SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis thalia
sp|P47192|VA722_ARATH G Vesicle-associated membrane protein 722 (AtVAMP722) (Sy
protein 1)
gb|AAL31896.1|AF419564_1 G At2g33120/F25I18.14 [Arabidopsis thaliana]
6 more sequence titles

gb|AAC04921.1| G putative synaptobrevin [Arabidopsis thaliana]
gb|AAL62414.1| G putative synaptobrevin [Arabidopsis thaliana]
gb|AAL79587.1| G At2g33120/F25I18.14 [Arabidopsis thaliana]
gb|AAM48025.1| G putative synaptobrevin [Arabidopsis thaliana]
gb|AAM64431.1| G putative synaptobrevin [Arabidopsis thaliana]
gb|AAM91096.1| G At2g33120/F25I18.14 [Arabidopsis thaliana]
Length=221

GENE ID: 817874 SAR1 | SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)
[Arabidopsis thaliana] (10 or fewer PubMed links)

```
 Score =  369 bits (946),  Expect = 9e-101, Method: Compositional matrix adjust.
 Identities = 188/219 (85%), Positives = 206/219 (94%), Gaps = 0/219 (0%)

Query  1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNCDGHTFNYLVE
Sbjct  1    MAQQSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNCDGHTFNYLVE   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVVAV+S G+QIP+AF++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY
Sbjct  61   NGFTYCVVAVDSAGRQIPMAFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+DHP E+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR QG
Sbjct  121  CMDHPDEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILS+C GF C  219
            T +RRKMW QNMKIKLIVL IIIALILIIILS+C GF C
Sbjct  181  TQMRRKMWFQNMKIKLIVLAIIIALILIIILSICGGFNC  219
```

>gb|AAA56991.1| formerly called HAT24; synaptobrevin-related protein
Length=221

```
 Score =  365 bits (938),  Expect = 8e-100, Method: Compositional matrix adjust.
 Identities = 187/219 (85%), Positives = 205/219 (93%), Gaps = 0/219 (0%)

Query  1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNCDGHTFNYLVE
Sbjct  1    MAQQSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNCDGHTFNYLVE   60
```

```
Query   61    DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY   120
              +GFTYCVVAV+S G+QIP+AF++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY
Sbjct   61    NGFTYCVVAVDSAGRQIPMAFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY   120

Query  121    CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG   180
              C+ HP+E+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR QG
Sbjct  121    CMAHPDEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTQG   180

Query  181    TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC               219
              T +RRKMW QNMKIKLIVL IIIALILIIILS+C GF C
Sbjct  181    TQMRRKMWFQNMKIKLIVLAIIIALILIIILSICGGFNC               219
```

>ref|NP_001031469.1| [UG] SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis tha
Length=229

 GENE ID: 817874 SAR1 | SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)
[Arabidopsis thaliana] (10 or fewer PubMed links)

 Score = 360 bits (925), Expect = 3e-98, Method: Compositional matrix adjust.
 Identities = 187/227 (82%), Positives = 206/227 (90%), Gaps = 8/227 (3%)

```
Query    1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
             M QQSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNCDGHTFNYLVE
Sbjct    1    MAQQSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNCDGHTFNYLVE   60

Query   61    DGFT--------YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGS   112
             +GF+        YCVVAV+S G+QIP+AF++RVKEDF KRYGGGKAATA ANSLN+EFGS
Sbjct   61    NGFSESKYCSISYCVVAVDSAGRQIPMAFLERVKEDFNKRYGGGKAATAQANSLNKEFGS   120

Query  113    KLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQ   172
             KLKEHMQYC+DHP+E+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQ
Sbjct  121    KLKEHMQYCMDHPDEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQ   180

Query  173    AQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC               219
             AQDFR QGT +RRKMW QNMKIKLIVL IIIALILIIILS+C GF C
Sbjct  181    AQDFRTQGTQMRRKMWFQNMKIKLIVLAIIIALILIIILSICGGFNC               227
```

>gb|ABK92923.1| unknown [Populus trichocarpa]
 gb|ABK94486.1| unknown [Populus trichocarpa]
 gb|ABK95420.1| unknown [Populus trichocarpa]
Length=221

 Score = 357 bits (917), Expect = 2e-97, Method: Compositional matrix adjust.
 Identities = 179/219 (81%), Positives = 201/219 (91%), Gaps = 0/219 (0%)

```
Query    1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
             M Q+SLIYAFV+RGTVILAE+TEF+GNF +IA QCL KLPA+NNKFTYNCDGHTFNYL +
Sbjct    1    MNQKSLIYAFVSRGTVILAEFTEFSGNFNSIAFQCLQKLPATNNKFTYNCDGHTFNYLAD   60

Query   61    DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY   120
             +GFTYCVVA ES G+Q+P+AF++RVK+DF +YGGGKAATA AN LN+EFG KLKEHM+Y
Sbjct   61    NGFTYCVVADESAGRQVPMAFLERVKDDFVSKYGGGKAATAQANGLNKEFGPKLKEHMKY   120

Query  121    CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG   180
             C DHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENL SQAQDFR QG
Sbjct  121    CADHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLHSQAQDFRSQG   180

Query  181    TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC               219
             T +RRKMWLQNMK+KLIVLGI+IALILII+LSVC GF C
Sbjct  181    TQIRRKMWLQNMKVKLIVLGILIALILIIVLSVCKGFNC               219
```

>gb|EAZ03095.1| hypothetical protein OsI_024327 [Oryza sativa (indica cultivar-g
 gb|EAZ39005.1| hypothetical protein OsJ_022488 [Oryza sativa (japonica cultivar
Length=279

 Score = 357 bits (915), Expect = 4e-97, Method: Compositional matrix adjust.
 Identities = 211/278 (75%), Positives = 217/278 (78%), Gaps = 59/278 (21%)

```
Query    1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
             MGGQSLIYAFVARGTV+LAEYTEFTGNFTTIA+QCL KLPASNNKFTYNCDGHTFNYLVE
Sbjct    1    MGGQSLIYAFVARGTVVLAEYTEFTGNFTTIAAQCLQKLPASNNKFTYNCDGHTFNYLVE   60
```

```
Query   61   DGFT------------YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLN   107
             DGF+            YCVVAVESVG+QIPIAF+DRVKEDFTKRYGGGKAATAAANSLN
Sbjct   65   DGFSSNRIGILGIQGLAYCVVAVESVGRQIPIAFLDRVKEDFTKRYGGGKAATAAANSLN   120

Query  108   REFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTE   167
             REFGSKLKEHMQYCVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTE
Sbjct  121   REFGSKLKEHMQYCVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTE   180

Query  168   NLRSQ------------------------------------AQDFRQQGT   181
             NLRSQ                                    AQDFRQQGT
Sbjct  181   NLRSQNSGIFIQWIAMEKLLIHVSVDRMRVWSMVMKYRIMVPKVIWLTVDMAQDFRQQGT   240

Query  182   NVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   219
              VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC
Sbjct  241   KVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   278
```

>gb|EAZ28954.1| hypothetical protein OsJ_012437 [Oryza sativa (japonica cultivar
Length=346

 Score = 351 bits (901), Expect = 2e-95, Method: Compositional matrix adjust.
 Identities = 176/189 (93%), Positives = 182/189 (96%), Gaps = 0/189 (0%)

```
Query    1   MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
             MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE
Sbjct    1   MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60

Query   61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY   120
             DGFTYCVVAVESVG+QIPIAF+DRVK+DFTKRY GGKAATAAANSLNR+FGSKLKEHMQY
Sbjct   61   DGFTYCVVAVESVGRQIPIAFLDRVKDDFTKRYGGGKAATAAANSLNRDFGSKLKEHMQY   120

Query  121   CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG   180
             CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQ G
Sbjct  121   CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQAG   180

Query  181   TNVRRKMWL   189
             T   R+ L
Sbjct  181   TQGTRRQTL   189
```

>gb|EAY92225.1| hypothetical protein OsI_013458 [Oryza sativa (indica cultivar-g
Length=346

 Score = 351 bits (900), Expect = 2e-95, Method: Compositional matrix adjust.
 Identities = 176/189 (93%), Positives = 182/189 (96%), Gaps = 0/189 (0%)

```
Query    1   MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
             MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE
Sbjct    1   MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60

Query   61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY   120
             DGFTYCVVAVESVG+QIPIAF+DRVK+DFTKRY GGKAATAAANSLNR+FGSKLKEHMQY
Sbjct   61   DGFTYCVVAVESVGRQIPIAFLDRVKDDFTKRYGGGKAATAAANSLNRDFGSKLKEHMQY   120

Query  121   CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG   180
             CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQ G
Sbjct  121   CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQAG   180

Query  181   TNVRRKMWL   189
             T   R+ L
Sbjct  181   TQGTRRQTL   189
```

>emb|CAN65946.1| hypothetical protein [Vitis vinifera]
Length=200

 Score = 349 bits (896), Expect = 6e-95, Method: Compositional matrix adjust.
 Identities = 179/199 (89%), Positives = 192/199 (96%), Gaps = 0/199 (0%)

```
Query   21   YTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTYCVVAVESVGQQIPIA   80
             YTEFTGNFT+IA+QCL KLPASNNKFTYNCDGHTFNYLVE+GFTYCVVAVES G+QIPIA
Sbjct    2   YTEFTGNFTSIAAQCLQKLPASNNKFTYNCDGHTFNYLVENGFTYCVVAVESAGRQIPIA   61

Query   81   FMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSE   140
             F++RVK+DF KRYGGGKAATA AN LN+EFG KLKEHMQYCVDHPEE+SKLAKVKAQVSE
Sbjct   62   FLERVKDDFNKRYGGGKAATAVANGLNKEFGPKLKEHMQYCVDHPEEISKLAKVKAQVSE   121
```

```
Query  141  VKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLG  200
            VKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGT +RRKMW+QNMKIKLIVLG
Sbjct  122  VKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTKMRRKMWMQNMKIKLIVLG  181

Query  201  IIIALILIIILSVCHGFKC  219
            IIIALILII+LS+CHGFKC
Sbjct  182  IIIALILIIVLSICHGFKC  200
```

>gb|**ABK24294.1**| unknown [Picea sitchensis]
Length=221

 Score = 349 bits (895), Expect = 9e-95, Method: Compositional matrix adjust.
 Identities = 155/220 (70%), Positives = 192/220 (87%), Gaps = 0/220 (0%)

```
Query    1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE  60
            MG+QSLIY+FV+RGTVILAEYTEFTGNFTT+A QCL KLPA++NKFT++C  HTFNYLVE
Sbjct    1  MGEQSLIYSFVSRGTVILAEYTEFTTVAYQCLQKLPATSNKFTFDCQRHTFNYLVE  60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGFTYCVVA ESVG+Q+PIAF++R+K++F KRY  G+A  A AN LN+EFG KLK+HM Y
Sbjct   61  DGFTYCVVADESVGRQVPIAFLERIKDEFKKRYSDGRAEVAIANGLNQEFGPKLKQHMDY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C  HPE+++K AK KAQV+EVKGVMMM+NIEK+LDRGEKIEL+VDKTE L+ QAQDF++QG
Sbjct  121  CAQHPEQINKFAKTKAQVAEVKGVMMDNIEKILDRGEKIELMVDKTEQLQFQAQDFQKQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH  220
            T +RRKMW +NMK+KLI L  ++ +IL+I +S+C GFKCH
Sbjct  181  TQIRRKMWFRNMKVKLICLSFLLFVILMIWISLCRGFKCH  220
```

>ref|**NP_001049070.1**| 🆄🅶 Os03g0165800 [Oryza sativa (japonica cultivar-group)]

 gb|**ABF94152.1**| 🅶 Vesicle-associated membrane protein 724, putative, expressed
[Oryza sativa (japonica cultivar-group)]

 dbj|**BAF10984.1**| 🅶 Os03g0165800 [Oryza sativa (japonica cultivar-group)]
 gb|**EAY88679.1**| hypothetical protein OsI_009912 [Oryza sativa (indica cultivar-g
Length=223

 GENE ID: 4331733 Os03g0165800 | Os03g0165800 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score = 346 bits (887), Expect = 7e-94, Method: Compositional matrix adjust.
 Identities = 152/217 (70%), Positives = 188/217 (86%), Gaps = 0/217 (0%)

```
Query    3  QQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDG  62
            + +L+Y+FVARG V+LA++ E +GNF ++A+QCL KLP++NN+ +YNCDGHTFNY V DG
Sbjct    6  RTTLVYSFVARGAVVLADHAEVSGNFASVAAQCLQKLPSTNNRHSYNCDGHTFNYHVHDG  65

Query   63  FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
            FTYCVVA ES G+Q+P+ F++RVKEDF+K+Y SGGKAKNATANSLKREYGPKLKEHMKYCD
Sbjct   66  FTYCVVATESAGRQLPVGFIERVKEDFSKKYSGGKAKNATANSLKREYGPKLKEHMKYCD  125

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
            +HPEE+ KLAKVKAQV+EVKGVMM+NIEKVLDRGEKIELLVDKTE+LRSQAQDFR+ GT
Sbjct  126  AHPEEIDKLAKVKAQVTEVKGVMMQNIEKVLDRGEKIELLVDKTEDLRSQAQDFRKAGTK  185

Query  183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            +RRKMW +NMK+KLIV GI+ALIL+IIL+VC    C
Sbjct  186  IRRKMWWENMKMKLIVFGIVVALILVIILTVCRDLNC  222
```

>ref|**XP_001777330.1**| 🆄🅶 R-SNARE, VAMP72-family [Physcomitrella patens subsp. pa

 gb|**EDQ57860.1**| 🅶 R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]
Length=222

 Score = 326 bits (835), Expect = 8e-88, Method: Compositional matrix adjust.
 Identities = 157/219 (71%), Positives = 191/219 (87%), Gaps = 0/219 (0%)

```
Query    1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE  60
            MG QSLIY+FVARG+ +LAEYT F+GNF+TIA QCL KLP +NNKFTY CD HTFNYLVE
```

```
Sbjct    1  MGTQSLIYSFVARGSTVLAEYTAFSGNFSTIAVQCLQKLPPNNNKFTYTCDRHTFNYLVE   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +G+TY VVA E  G+QIP AF++RVKEDF +RY GGKA +A ANSL++EFG KLK+HMQY
Sbjct   61  EGYTYLVVADEEFGRQIPFAFLERVKEDFKRRYAGGKADSAIANSLDKEFGPKLKDHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEBKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            CVDHP+E++K+K+K+QV+EVKG+MM+NIEKVLDRGEKIELLVDKTENLR QA +F++QG
Sbjct  121  CVDHPDEMNKISKIKSQVAEVKGIMMMDNIEKVLDRGEKIELLVDKTENLRFQADNFQRQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            +RRKMW QNMK+KLIVL III +I+II LS+C GF C
Sbjct  181  KQLRRKMWFQNMKVKLVLAIIIVIIIIIWLSICRGFTC  219


>emb|CAO70980.1|  unnamed protein product [Vitis vinifera]
Length=221

 Score =  325 bits (833),  Expect = 1e-87, Method: Compositional matrix adjust.
 Identities = 151/219 (68%), Positives = 187/219 (85%), Gaps = 0/219 (0%)

Query    1  MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M Q+S IY+FVARGT++LAEYTEFTGNF  IA+QCL +LP++NNKFTYNCD HTFN+LVE
Sbjct    1  MSQESFIYSFVARGTMVLAEYTEFTGNFPAIATQCLQRLPSANNKFTYNCDHHTFNFLVE   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DG+ YCVVA ESVG+Q+ IAF++R+K DF KRYGGGKA TA A SLN++FG   +KEHMQY
Sbjct   61  DGYAYCVVAAESVGKQVSIAFLERMKADFKKRYGGGKADTATAKSLNKDFGPIMKDHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEBKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            +DH EE+ KL KVKAQVSEVK +M+ENI+K L+RGE + +L DKTE+LRSQAQ F++QG
Sbjct  121  IIDHAEEIEKLLKVKAQVSEVKSIMLENIDKTILADKTEDLRSQAQQFKKQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            + VRRKMW QNMKIKL+VLGI++ L L+I +S+CHGF C
Sbjct  181  SQVRRKMWFQNMKIKLVVLGILLILALVIWVSICHGFNC  219


>gb|ABK27118.1|  unknown [Picea sitchensis]
Length=219

 Score =  325 bits (832),  Expect = 2e-87, Method: Compositional matrix adjust.
 Identities = 144/220 (65%), Positives = 189/220 (85%), Gaps = 1/220 (0%)

Query    1  MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSLIY+FVARG ++LAE+T F+GNF+ IA QCL KLP+++NKFTY CD HTFNYLV+
Sbjct    1  MAQQSLIYSFVARGNIVLAEHTSFSGNFSIIAVQCLQKLPSNSNKFTYTCDNHTFNYLVD   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGF + VV+ E+ G+Q+P  F++RVKEDF +RYGG +A T+ A+SL++++G  L++HMQY
Sbjct   61  DGFVFLVVSDEAAGRQVPFLFLERVKEDFKRRYGG-RAETSMAHSLDKDYGPILRDHMQY  119

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEBKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+DHPEE+SK +K+KAQVSEVKG+MM+NIEKVLDRGEKIELLVDKTE L+ QA +F++QG
Sbjct  120  CMDHPEELSKFSKIKAQVSEVKGIMMMDNIEKVLDRGEKIELLVDKTEGLQFQADNFQRQG  179

Query  181  TNVRRKMWLQNMKILKLIVLGIIIALILIIILSVCHGFKCH  220
            +RRKMWLQN+K K+IVLG ++++ILII LSVC GF C+
Sbjct  180  RQLRRKMWLQNLKFKIIVLGTVLSIILIIWLSVCKGFSCN  219


>gb|ABK23325.1|  unknown [Picea sitchensis]
Length=235

 Score =  319 bits (818),  Expect = 6e-86, Method: Compositional matrix adjust.
 Identities = 148/236 (62%), Positives = 189/236 (80%), Gaps = 17/236 (7%)

Query    1  MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSLIY+FVARG ++LAE+T F+GNF+ IA QCL KLP+++NKFTY CD HTFNYLV+
Sbjct    1  MAQQSLIYSFVARGNIVLAEHTSFSGNFSIIAVQCLQKLPSNSNKFTYTCDNHTFNYLVD   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLN------------  107
            DGF + VVA E+ G+Q+P  F++RVKEDF +RYGG +A T+ A+SL+
Sbjct   61  DGFVFLVVSDEAAGRQVPFLFLERVKEDFKRRYGG-RAETSMAHSLDKDYGYEEKFSVAY  119

Query  108  ---REFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEBKVLDRGEKIELLVD  164
```

```
              REFG  L++HMQYC+DHPEE+SK  +K+KAQVSEVKG+MM+NIEKVLDRGEKIELLVD
Sbjct  120   NLDREFGPILRDHMQYCMDHPEELSKFSKIKAQVSEVKGIMMDNIEKVLDRGEKIELLVD   179

Query  165   KTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH      220
             KTE L+ QA +F++QG  +RRKMWLQN+K K+IVLG ++++ILII LSVC GF C+
Sbjct  180   KTEGLQFQADNFQRQGRQLRRKMWLQNLKFKIIVLGTVLSIILIIWLSVCKGFSCN      235
```

>sp|O23429|VA724_ARATH Vesicle-associated membrane protein 724 (AtVAMP724) (SYBL
protein)
 gb|AAT41760.1| At4g15780 [Arabidopsis thaliana]
 gb|AAT70463.1| At4g15780 [Arabidopsis thaliana]
Length=222

 Score = 318 bits (815), Expect = 2e-85, Method: Compositional matrix adjust.
 Identities = 156/220 (70%), Positives = 190/220 (86%), Gaps = 1/220 (0%)

```
Query  1     MGGQQSLIYAFVARGTVILABYTEFTGNFTTIASQCLMKLPASNN-KFTYNCDGHTFNYLV   59
             MGQ+S IY+FVARGT+ILAEYTEFTGNFPSIAAQCLQKLPSSSNSKFTYNCDHHTFNFLV
Sbjct  1     MGQESFIYSFVARGTMILAEYTEFTGNFPSIAAQCLQKLPSSSNSKFTYNCDHHTFNFLV   60

Query  60    EDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQ  119
             EDG+ YCVVA +S+ +QI IAF++RVK DF KRYGGGKA+TA A SLN+EFG   +KEHM
Sbjct  61    EDGYAYCVVAKDSLSKQISIAFLERVKADFKKRYGGGKASTAIAKSLNKEFGPVMKEHMN  120

Query  120   YCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQ  179
             Y VDH EE+ KL VKAQVSEVK +M+ENI+K +DRGE + +L DKTENLRSQAQ++++Q
Sbjct  121   YIVDHAEEIEKLIKVKAQVSEVKSIMLENIKAIDRGENLTVLTDKTENLRSQAQEYKKQ  180

Query  180   GTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC          219
             GT +VRRK+W QNMKIKL+VLGI++ L+LII +SVCHGF C
Sbjct  181   GTQVRRKLWYQNMKIKLVVLGILLLLVLIIWISVCHGFNC            220
```

>ref|XP_001784148.1| **UG** R-SNARE, VAMP72-family [Physcomitrella patens subsp. pa
 gb|EDQ51072.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]
Length=220

 Score = 317 bits (813), Expect = 3e-85, Method: Compositional matrix adjust.
 Identities = 156/219 (71%), Positives = 190/219 (86%), Gaps = 0/219 (0%)

```
Query  1     MGGQQSLIYAFVARGTVILABYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
             MG QSLIY+FVARG  +LAEYT F+GNF+TIA QCLQKLP PNNNKFTY TC DRHTFNYLVE
Sbjct  1     MGTGSLIYSFVARGPTVLAEYTAFSGNFSTIAVQCLQKLPPNNNKFTYTCDRHTFNYLVE   60

Query  61    DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
             +G+TY VVA E  G+QIP AF++RVKEDF +RY GGKA +A A+SL++EFG KLK+HMQY
Sbjct  61    EGYTYLVVADEEFGRQIPFAFLERVKEDFKRRYAGGKADSAIAHSLDKEFGPKLKDHMQY  120

Query  121   CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
             CVDHP+E+K++K+K+QV+EVKG+MM+NIEKVLDRGEKIELLVDKTENLR QA +F++QG
Sbjct  121   CVDHPDEMNKISKISQVAEVKGIMMDNIEKVLDKTENLRFQADNFQRQG           180

Query  181   TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC            219
             +RRKMW QNMK+KLIVL III +I+II LS+C GF C
Sbjct  181   RQLRRKMWFQNMKVKLIVLAIIIVVIIIIWLSICRGFTC            219
```

>gb|AAV49990.1| putative synaptobrevin/VAMP [Hordeum vulgare subsp. vulgare]
Length=215

 Score = 303 bits (777), Expect = 5e-81, Method: Compositional matrix adjust.
 Identities = 140/214 (65%), Positives = 181/214 (84%), Gaps = 0/214 (0%)

```
Query  6     LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY   65
             +IYA VARGTV++AE+T +TGNF  IA QCL HKLPAGDSRFAYNCDGHTFTFLLHQGYAY
Sbjct  1     MIYAMVARGTVVVAEHTAYTGNFRDIAGQCLHKLPAGDSRFAYNCDGHTFTFLLHQGYAY   60

Query  66    CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCMDHP  125
             CVVA ES G+++P+AF++R+KEDF +RY GGKAATA ANSL ++FG +LKE M+YC+DHP
Sbjct  61    CVVATESAGREVPLAFLERIKEDFNRRYAGGKAATAANSLTKDFGPRLKEQMNYCMDHP  120

Query  126   EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR  185
             EEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+I+ LV +TE L  A DFR +GT +RR
```

```
Sbjct  121  EEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIDGLVTRTEQLHDHALDFRTEGTRIRR  180

Query  186  KMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            +MW QNMKIKLIV+GI++ALILII+LS+CH   C
Sbjct  181  RMWYQNMKIKLIVVGIVVALILIIVLSICHKKDC  214
```

>gb|**ABK95406.1**| unknown [Populus trichocarpa]
Length=238

 Score = 293 bits (751), Expect = 4e-78, Method: Compositional matrix adjust.
 Identities = 133/235 (56%), Positives = 184/235 (78%), Gaps = 18/235 (7%)

```
Query    3  QQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDG   62
            Q+ LIY+FVA+G V+LAE+T ++GNF+TIA QCL KLP++++K+TY+ DGHTFN+L+++G
Sbjct    4  QKGLIYSFVAKGNVVLAEHTSYSGNFSTIAVQCLQKLPSNSSKYTYSSDGHTFNFLIDNG   63

Query   63  FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATA------------------AAN  104
            F + VVA ESVG+ +     F++RVK+DF +RYG     A             A      A
Sbjct   64  FVFLVVASVGRGVSFVFLERVKDDFNQRYGASIKNEAHPLADDDDDDDLFEDRFSIAY   123

Query  105  SLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVD  164
            +L+REFG +LKEHMQYCV+HPEE+SKL+K+KAQ++EVKG+MM+NI+KVLDRGE+IELLVD
Sbjct  124  NLDREFGPRLKEHMQYCVNHPEEISKLSKLKAQITEVKGIMMDNIDKVLDRGERIELLVD  183

Query  165  KTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILILIIILSVCHGFKC  219
            KT+NL  QA  F++QG  +RRKMWLQN+K+KL++ G ++ALI+I+ +SVC GFKC
Sbjct  184  KTDNLSFQADSFQRQGRELRRKMWLQNLKVKLVLGGTVLALIVIVWISVCGGFKC   238
```

>ref|**NP_190998.1**| 🇬 ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane
727)

 ref|**NP_001018283.1**| 🇺🇬 ATVAMP727 (Arabidopsis thaliana vesicle-associated memb
727)

 sp|**Q9M376|VA727_ARATH** 🇬 Vesicle-associated membrane protein 727 (AtVAMP727)

 emb|**CAB71004.1**| 🇬 synaptobrevin-like protein [Arabidopsis thaliana]

 gb|**AAS47612.1**| 🇬 At3g54300 [Arabidopsis thaliana]

 gb|**AAS76729.1**| 🇬 At3g54300 [Arabidopsis thaliana]

 dbj|**BAF00993.1**| 🇬 synaptobrevin -like protein [Arabidopsis thaliana]
Length=240

 GENE ID: 824597 ATVAMP727 | ATVAMP727 (Arabidopsis thaliana vesicle-associated
membrane protein 727) [Arabidopsis thaliana] (10 or fewer PubMed links)

 Score = 293 bits (751), Expect = 4e-78, Method: Compositional matrix adjust.
 Identities = 137/239 (57%), Positives = 181/239 (75%), Gaps = 21/239 (8%)

```
Query    1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M Q+ LIY+FVA+GTV+LAE+T ++GNF+TIA QCL KLP TNSSKYTYS CDGHTFNFLVD
Sbjct    1  MSQKGLIYSFVAKGTVVLAEHTPYSGNFSTIAVQCLQKLPTNSSKYTYSSCDGHTFNFLVD   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGG------------------GKAAT  100
            +GF + VVA ES G+ +P F++RVKEDF KRY               G   +
Sbjct   61  NGFVFLVVADESTGRSVPFVFLERVKEDFKKRYEASIKNDERHPLADEDEDDDLFGDRFS  120

Query  101  AAANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIE  160
             A N L+REFG  LKEHMQYC+ HPEE+SKL+K+KAQ++EVKG+MM+NIEKVLDRGEKIE
Sbjct  121  VAYN-LDREFGPILKEHMQYCMSHPEEMSKLSKLKAQITEVKGIMMDNIEKVLDRGEKIE  179

Query  161  LLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILILIIILSVCHGFKC  219
            LLVDKTENL+ QA  F++QG  +RRKMWLQ++++KL+ V G + +  ILI+ +  C GFKC
Sbjct  180  LLVDKTENLQFQADSFQRQGRQLRRKMWLQSLQMKLMVAGAVFSFILIVWVVACGGFKC   238
```

>ref|**NP_850201.1**| 🇺🇬 ATVAMP723 (Arabidopsis thaliana vesicle-associated membran
723)

 sp|**Q8VY69|VA723_ARATH** 🇬 Vesicle-associated membrane protein 723 (AtVAMP723)

 gb|**AAL62392.1**| 🇬 putative synaptobrevin [Arabidopsis thaliana]

```
  gb|AAN15528.1| G putative synaptobrevin [Arabidopsis thaliana]
Length=217

 GENE ID: 817873 ATVAMP723 | ATVAMP723 (Arabidopsis thaliana vesicle-associated
membrane protein 723) [Arabidopsis thaliana] (10 or fewer PubMed links)

 Score = 289 bits (739),  Expect = 1e-76, Method: Compositional matrix adjust.
 Identities = 155/219 (70%), Positives = 179/219 (81%), Gaps = 4/219 (1%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSL Y+F+ARGTVIL E+T+F GNFT++A+Q L  LP+SNNKFTYNCDGHTFN LVE
Sbjct  1    MAQQSLFYSFIARGTVILVEFTDFKGNFTSVAAQYLENLPSSNNKFTYNCDGHTFNDLVE   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVVAV+S G++IP+AF++RVKEDF KRYGG KAAT  ANSLN+EFGS LKEHMQY
Sbjct  61   NGFTYCVVAVDSAGREIPMAFLERVKEDFYKRYGGEKAATDQANSLNKEFGSNLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+DHP+E+S LAK KAQVSEVK +MMENIEKVL RG   E+L      SQ Q F   +
Sbjct  121  CMDHPDEISNLAKAKAQVSEVKSLMMENIEKVLARGVICEMLGSS----ESQPQAFYIKR  176

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T ++RK W QNMKIKLIVL IIIALILIIILSVC GF C
Sbjct  177  TQMKRKKWFQNMKIKLIVLAIIIALILIIILSVCGGFNC  215


>ref|NP_001062495.1| UG Os08g0558600 [Oryza sativa (japonica cultivar-group)]
 dbj|BAD13129.1| G putative vesicle-associated membrane protein 725 (AtVAMP725)
[Oryza sativa Japonica Group]
 dbj|BAF24409.1| G Os08g0558600 [Oryza sativa (japonica cultivar-group)]
Length=241

 GENE ID: 4346309 Os08g0558600 | Os08g0558600 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score = 286 bits (732),  Expect = 7e-76, Method: Compositional matrix adjust.
 Identities = 133/237 (56%), Positives = 177/237 (74%), Gaps = 20/237 (8%)

Query  3    QQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDG   62
            +QSLIY+FVA+G+V+LAE+T F+GNF+TIA QCL KLP +K TY+CDGHTFN+LV+ G
Sbjct  5    KQSLIYSFVAKGSVVLAEHTAFSGNFSTIAVQCLQKLPPNTSKSTYSCDGHTFNFLVDRG   64

Query  63   FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGG--------------------KAATAA  102
            F + VVA E+VG+ +P  F+DRVKEDF +RYG                      + +
Sbjct  65   FVFLVVADEAVGRSVPFVFLDRVKEDFMQRYGSSIDEEGQHPLADDADDDDFLLEDRFSI  124

Query  103  ANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELL  162
            A +L+REFG +LK+HM YC++HPEE+SKL+KVKA ++EVKG+MM+NIEK+L+RGEKIELL
Sbjct  125  AYNLDREFGPRLKDHMLYCINHPEEISKLSKVKAHLTEVKGIMMDNIEKILERGEKIELL  184

Query  163  VDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            V KTE L+SQA  F + G +RRKMWLQN++ KL+V G + ALIL + L +C GPKC
Sbjct  185  VGKTETLQSQADSFHRHGRELRRKMWLQNLRFKLMVGGAVAALILFLWLIICGGFKC  241


>emb|CAO63919.1| unnamed protein product [Vitis vinifera]
Length=239

 Score = 285 bits (728),  Expect = 2e-75, Method: Compositional matrix adjust.
 Identities = 138/239 (57%), Positives = 185/239 (77%), Gaps = 20/239 (8%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M Q+ LIY+FVA+GTV+LAE+T F+GNF+TIA QCL KLP++++K+TY+CDGHTFN+L++
Sbjct  1    MSQKGLISYFVAKGTVVLAEHTSFSGNFSTIAVQCLQKLPSNSSKYTYSCDGHTFNFLID   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAA------------------  102
             GF + VVA ES G+  P  F++RVK+DF +RYGG
Sbjct  61   SGFVFLVVADESAGRGAPFVFLERVKDDFKQRYGGSIRSDGPHPLADEDDDDDDLFEDRF  120

Query  103  --ANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIE  160
              A +L+REFG KLKEHMQYC++HPEE+SKL+K+KAQ++EVKG+MM+NIEKVLDRGERIE
Sbjct  121  SIAYNLDREFGPKLKEHMQYCMNHPEEISKLSKLKAQITEVKGIMMDNIEKVLDRGERIE  180
```

```
Query  161   LLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   219
             LLVDKTENL+ QA  F++QG  +RRKMWLQN+++KL+V GI++ LI+I+ L  C GFKC
Sbjct  181   LLVDKTENLQFQADSFQRQGRQLRRKMWLQNLRLKLMVGGIVLVLIIILWLIACKGFKC   239
```

>emb|CAJ15414.1| unnamed protein product [Triticum aestivum]
Length=231

Score = 283 bits (724), Expect = 5e-75, Method: Compositional matrix adjust.
Identities = 139/215 (64%), Positives = 183/215 (85%), Gaps = 0/215 (0%)

```
Query   5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             ++IYA VARGT+++AE+T +TGNF  IA+QCL KLPA +++FTY CDGHTF +L+  G+
Sbjct  16   TMIYAMVARGTLVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHTFTFLLHQGYA   75

Query  65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            YCVVA ES G+++P+AF+++R+KE+F KRY GGKAATA ANSL+++FG +LKE MQYC+DH
Sbjct  76   YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLSKDFGPRLKEQMQYCMDH  135

Query  125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+I+ LV +TE L    A DFR +GT +R
Sbjct  136  PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIDGLVTRTEQLHDHAMDFRTEGTRLR  195

Query  185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   219
            R+MW QNMKIKLIV GI++A+ILII+LS+CH    C
Sbjct  196  RRMWYQNMKIKLIVAGIVVAIILIIVLSICHRDHC   230
```

>emb|CAJ13968.1| unnamed protein product [Aegilops tauschii]
Length=231

Score = 283 bits (723), Expect = 7e-75, Method: Compositional matrix adjust.
Identities = 139/215 (64%), Positives = 183/215 (85%), Gaps = 0/215 (0%)

```
Query   5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             ++IYA VARGT+++AE+T +TGNF  IA+QCL KLPA +++FTY CDGHTF +L+  G+
Sbjct  16   TMIYAMVARGTLVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHTFTFLLHQGYA   75

Query  65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            YCVVA ES G+++P+AF+++R+KE+F KRY GGKAATA ANSL+++FG +LKE MQYC+DH
Sbjct  76   YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLTKDFGPRLKEQMQYCMDH  135

Query  125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+I+ LV +TE L    A DFR +GT +R
Sbjct  136  PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIDGLVTRTEQLHDHAMDFRTEGTRLR  195

Query  185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   219
            R+MW QNMKIKLIV GI++A+ILII+LS+CH    C
Sbjct  196  RRMWYQNMKIKLIVAGIVVAIILIIVLSICHRDHC   230
```

>emb|CAJ13552.1| unnamed protein product [Triticum turgidum]
Length=232

Score = 283 bits (723), Expect = 8e-75, Method: Compositional matrix adjust.
Identities = 139/215 (64%), Positives = 181/215 (84%), Gaps = 0/215 (0%)

```
Query   5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             ++IYA VARGT+++AE+T +TGNF  IA+QCL KLPA +++FTY CDGH F +L+  G+
Sbjct  16   TMIYAMVARGTMVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHAFTFLLHQGYA   75

Query  65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            YCVVA ES G+++P+AF+++R+KE+F KRY GGKAATA ANSL+++FG +LKE MQYC+DH
Sbjct  76   YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLTKDFGPRLKEQMQYCMDH  135

Query  125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+IE LV  +TE L   A DFR +GT +R
Sbjct  136  PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIEGLVTRTEQLHDHALDFRTEGTRIR  195

Query  185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   219
            R+MW QNMKIKLIV GI++A+ILI+LS+CH    C
Sbjct  196  RRMWYQNMKIKLIVAGIVVAIILIIVLSICHRDHC   230
```

>emb|CAJ13539.1| unnamed protein product [Triticum aestivum]
Length=232

```
 Score = 282 bits (722),  Expect = 1e-74, Method: Compositional matrix adjust.
 Identities = 139/215 (64%), Positives = 181/215 (84%), Gaps = 0/215 (0%)

Query  5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
            ++IYA VARGT+++AE+T +TGNF  IA+QCL KLPA +++FTY CDGH F +L+  G+
Sbjct  16   TMIYAMVARGTMVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHAFTFLLHQGYA  75

Query  65   YCVVAVESVGGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            YCVVA ES G+++P+AF++R+KE+F KRY GGKAATA ANSL ++FG +LK+ MQYC+DH
Sbjct  76   YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLTKDFGPRLKEQMQYCMDH  135

Query  125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+IE LV +TE L   A DFR +GT +R
Sbjct  136  PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIEGLVTRTEQLHDHALDFRTEGTRIR  195

Query  185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            R+MW QNMKIKLIV GI++A+ILII+LS+CH   C
Sbjct  196  RRMWYQNMKIKLIVAGIVVAIILIIVLSICHRDHC  230
```

>gb|AAS88558.1| putative synaptobrevin [Triticum monococcum]
Length=218

```
 Score = 281 bits (719),  Expect = 2e-74, Method: Compositional matrix adjust.
 Identities = 138/215 (64%), Positives = 181/215 (84%), Gaps = 0/215 (0%)

Query  5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
            ++IYA VARGT+++AE+T +TGNF  IA+QCL KLPA +++FTY CDGH F +L+  G+
Sbjct  2    TMIYAMVARGTMVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHAFTFLLHQGYA  61

Query  65   YCVVAVESVGGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            YCVVA ES G+++P+AF++R+KE+F KRY GGKAATA ANSL ++FG +LK+ MQYC+DH
Sbjct  62   YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLTKDFGPRLKDQMQYCMDH  121

Query  125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+IE LV +TE L   A DFR +GT +R
Sbjct  122  PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIEGLVTRTEQLHDHALDFRTEGTRIR  181

Query  185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            R+MW QNMKIKLIV GI++A+ILII+LS+CH   C
Sbjct  182  RRMWYQNMKIKLIVAGIVVAIILIIVLSICHRDHC  216
```

>ref|NP_001030968.1| UG VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabid
thaliana]

  dbj|BAD44122.1| G putative vesicle-associated membrane protein, synaptobrevin 7
[Arabidopsis thaliana]
Length=181

 GENE ID: 839419 VAMP7B | VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B)
[Arabidopsis thaliana] (10 or fewer PubMed links)

```
 Score = 280 bits (716),  Expect = 6e-74, Method: Compositional matrix adjust.
 Identities = 155/219 (70%), Positives = 170/219 (77%), Gaps = 38/219 (17%)

Query  1    MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE  60
            M QQSLIY+FVARGTVIL E+T+F
Sbjct  1    MAQQSLIYSFVARGTVILVEFTDFKA----------------------------------  26

Query  61   DGFTYCVVAVESVGGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
                YCVVAV+S G+QIP+++F++RVKEDF KRYGGGKAATA QANSLNKEFGSKLKEHMQY
Sbjct  27   ----YCVVAVDSAGRQIPMSFLERVKEDFNKRYAGGKAATAQANSLNKEFGSKLKEHMQY  82

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+DHP+E+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR  G
Sbjct  83   CMDHPDEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTTG  142

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T +RRKMWLQNMKIKLIVL IIIALILII+LSVCHGFKC
Sbjct  143  TQMRRKMWLQNMKIKLIVLAIIIALILIIVLSVCHGFKC  181
```

```
>ref|XP_001779971.1| G R-SNARE, VAMP72-family [Physcomitrella patens subsp. pate
  gb|EDQ55180.1| G R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]
Length=239

 Score =  278 bits (711),  Expect = 2e-73, Method: Compositional matrix adjust.
 Identities = 132/220 (60%), Positives = 174/220 (79%), Gaps = 0/220 (0%)

Query  1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MG +LIY+ V+RGT +LAEYT F GNF+ IA QCL+KLPA+NNK TY  D HTFN+LV+
Sbjct  1    MGDANLIYSLVSRGTTVLAEYTSFAGNFSQIAMQCLVKLPAANNKHTYVMDRHTFNFLVQ   60

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DGFTY VVA E  G+QIP AF+DRVK+DF  RY GGKA A ++SL+ EFG +LKEHM +
Sbjct  61   DGFTYLVVAEEDFGRQIPFAFLDRVKDDFKHRYQGGKADLAVSHSLDAEFGPRLKEHMDF  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C  +PEE+ K++K+K+QV+EVKG+MMENI+KVL R EKI+LLVD+T +L+S A +F++QG
Sbjct  121  CERNPEEIRKMSKIKSQVAEVKGIMMENIDKVLVRNEKIDLLVDRTSHLQSDAHNFQRQG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH                      220
            +R K+W QN ++KL+VL +II +  II LS+C GF C+
Sbjct  181  KKIRYKLWCQNYRLKLLVLVLIIIVAFIIYLSICRGFVCY                      220


>ref|NP_193313.2| UG ATVAMP724 (Arabidopsis thaliana vesicle-associated membran
724)
Length=194

 GENE ID: 827258 ATVAMP724 | ATVAMP724 (Arabidopsis thaliana vesicle-associated
membrane protein 724) [Arabidopsis thaliana] (10 or fewer PubMed links)

 Score =  275 bits (702),  Expect = 2e-72, Method: Compositional matrix adjust.
 Identities = 158/189 (67%), Positives = 158/189 (83%), Gaps = 2/189 (1%)

Query  1    MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASN-KFTYNCDGHTFNYLV   59
            MGQ+S IY+FVARGT+ILAEYTEFTGNF SIAAQCLQKLPSSNSKFTYNCDHHTFNFLV
Sbjct  1    MGQESFIYSFVARGTMILAEYTEFTGNFPSIAAQCLQKLPSSNSKFTYNCDHHTFNFLV   60

Query  60   EDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQ  119
            ED + YCVVA +S+ +QI IAF++RVK DF KRYGGGKA+TAIAKSLNKEFGPVMKEHMN
Sbjct  61   EDAYAYCVVAKDSLSKQISIAFLERVKADFKKRYGGGKASTAIAKSLNKEFGPVMKEHMN  120

Query  120  YCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQ-  178
            Y VDH EE+ KL KVKAQVSEVK +M+ENI+K +DRGE +L DKTENLRSQA++++
Sbjct  121  YIVDHAEEIEKLIKVKAQVSEVKSIMLENIDKAIDRGENLTVLTDKTENLRSQAREYKKT  180

Query  179  QGTNVRRKM  187
            +G   RRK
Sbjct  181  KGHRWRRKF  189


>ref|XP_001692216.1| UG R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt
  gb|EDP04166.1| G R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]
Length=219

 GENE ID: 5717909 VAMP72 | R-SNARE protein, VAMP72-family
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

 Score =  268 bits (685),  Expect = 2e-70, Method: Compositional matrix adjust.
 Identities = 126/210 (60%), Positives = 167/210 (79%), Gaps = 1/210 (0%)

Query  5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
            LIYAFVARGT +LAEYT ++GNF T+A +CL KL    KFT CD HTFN+LV +GFT
Sbjct  2    PLIYAFVARGTTVLAEYTPYSGNFNTVAIECLQKLANPEPKFTIACDRHTFNFLVANGFT   61

Query  65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            Y VVA E+ G+QIP AF++RV+++F ++   KA TAAA S++R FG +LK HM+YCVDH
Sbjct  62   YLVVADEAYGRQIPFAFLERVRDEFEEKYAE-KARTAAALSMDRTFGPRLKSHMEYCMDH  120

Query  125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            PEE+SK+A V+ +V+EVK VM+ENIEKVL+RGEKIELLVDKT+DLRNQAEQFQKKGRQLR
Sbjct  121  PEEISKIAAVQKKVNEVKDVMVENIEKVLERGEKIELLVDKTDDLRNQAEQFQKKGRQLR  180
```

```
Query  185  RKMWLQNMKIKLIVLGIIIALILIIILSVC  214
            KMW QN ++KLIVL  I+ L ++I L VC
Sbjct  181  NKMWWQNCRMKLIVLFAILLLAVVIFLLVC  210
```

>ref|NP_001059291.1| **UG** Os07g0249200 [Oryza sativa (japonica cultivar-group)]

dbj|BAC20811.1| **G** putative Vesicle-associated membrane protein [Oryza sativa Ja Group]

dbj|BAD30660.1| **G** putative Vesicle-associated membrane protein [Oryza sativa Ja Group]

dbj|BAF21205.1| **G** Os07g0249200 [Oryza sativa (japonica cultivar-group)]
Length=248

 GENE ID: 4342836 Os07g0249200 | Os07g0249200 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score = 266 bits (679), Expect = 9e-70, Method: Compositional matrix adjust.
 Identities = 135/223 (60%), Positives = 175/223 (78%), Gaps = 9/223 (4%)

```
Query   6  LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNN---------KFTYNCDGHTFN  56
           LIYAFVARGT +LAEYTEFTGNF  +A+QCL +LPAS          +F+Y CDGHTFN
Sbjct  23  LIYAFVARGTAVLAEYTEFTGNFPALAAQCLQRLPASGGGGSGGGAPARFSYACDGHTFN  82

Query  57  YLVEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKE  116
           +L+  G+ YCVVA ESV + + +AF++R+K+DF KRYGGGKA TA A SLN+E+G  +K+
Sbjct  83  FLLHRGYAYCVVAKESVPKNVSVAFLERLKDDFMKRYGGGKADTALAKSLNKEYGPVIKQ  142

Query 117  HMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDF  176
           HMQY +DH EE+ K  KV+AQVSEVK +M+ENIEK L RGEK+ L DKT +L+SQAQ+F
Sbjct 143  HMQYVLDHSEEIEKTLKVQAQVSEVKNIMLENIEKTLGRGEKLSELQDKTSDLQSQAQEF  202

Query 177  RQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
           +++G +RRK WLQNMKIKL+VLGI++ L++I+ +SVC GF C
Sbjct 203  KKKGVKIRRKTWLQNMKIKLVVLGILLLLVIIVWVSVCQGFDC  245
```

>gb|EAZ07996.1| hypothetical protein OsI_029228 [Oryza sativa (indica cultivar-g
Length=633

 Score = 263 bits (673), Expect = 5e-69, Method: Compositional matrix adjust.
 Identities = 121/216 (56%), Positives = 162/216 (75%), Gaps = 20/216 (9%)

```
Query   2  GQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDG  61
           +QSLIY+FVA+G+V+LAE+T F+GNF+TIA QCL KLP + +K TY+CDGHTFN+LV+
Sbjct   4  NKQSLIYSFVAKGSVVLAEHTAFSGNFSTIAVQCLQKLPPNTSKSTYSCDGHTFNFLVDR  63

Query  62  GFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGG--------------------KAATA  101
           GF + VVA E+VG+ +P  F+DRVKEDF +RYG                     KAATA
Sbjct  64  GFVFLVVADEAVGRSVPFVFLDRVKEDFMQRYGSSIDEEGQHPLADDADDDDFLLEDRFS  123

Query 102  AANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIEL  161
            A  +L+REFG +LK+HM YC++H+PEE+ SKLSKV KVKA ++EVKG+MMDNIEKILERGEKIEL
Sbjct 124  IAYNLDREFGPRLKDHMLYCINHPEEISKLSKVKAHLTEVKGIMMDNIEKILERGEKIEL  183

Query 162  LVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLI  197
           LV KTE L+SQA  F + G  +RRKMWLQN++ KL+
Sbjct 184  LVGKTETLQSQADSFHRHGRELRRKMWLQNLRFKLM  219
```

>gb|EAZ43645.1| hypothetical protein OsJ_027128 [Oryza sativa (japonica cultivar
Length=1259

 Score = 263 bits (672), Expect = 7e-69, Method: Compositional matrix adjust.
 Identities = 121/215 (56%), Positives = 162/215 (75%), Gaps = 20/215 (9%)

```
Query   3  QQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDG  62
           +QSLIY+FVA+G+V+LAE+T F+GNF+TIA QCL KLP + +K TY+CDGHTFN+LV+ G
Sbjct   5  KQSLIYSFVAKGSVVLAEHTAFSGNFSTIAVQCLQKLPPNTSKSTYSCDGHTFNFLVDRG  64

Query  63  FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGG-------------------KAATAA  102
           F + VVA E+VG+ +P  F+DRVKEDF +RYG                     + +
Sbjct  65  FVFLVVADEAVGRSVPFVFLDRVKEDFMQRYGSSIDEEGQHPLADDADDDDFLLEDRFSI  124
```

```
Query  103  ANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELL  162
            A +L+REFG +LK+HM YC++HPEE+SKL+KVKA ++EVKG+MM+NIEK+L+RGEKIELL
Sbjct  125  AYNLDREFGPRLKDHMLYCINHPEEISKLSKVKAHLTEVKGIMMDNIEKILERGEKIELL  184

Query  163  VDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLI  197
            V KTE L+SQA  F + G  +RRKMWLQN++ KL+
Sbjct  185  VGKTETLQSQADSFHRHGRELRRKMWLQNLRFKLM  219


>gb|AAC04922.1|  putative synaptobrevin [Arabidopsis thaliana]
Length=212

  Score =  261 bits (668),  Expect = 2e-68, Method: Compositional matrix adjust.
  Identities = 121/163 (74%), Positives = 142/163 (87%), Gaps = 0/163 (0%)

Query    1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M QQSL Y+F+ARGTVIL E+T+F GNFT++A+Q L  LP+SNNKFTYNCDGHTFN LVE
Sbjct    1  MAQQSLFYSFIARGTVILVEFTDFKGNFTSVAAQYLENLPSSNNKFTYNCDGHTFNDLVE   60

Query   61  DGFTYCVVAVESVGQQIPIAPMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFTYCVVAV+S G++IP+AF++RVKEDF KRYGG KAAT  ANSLN+EFGS LKEHMQY
Sbjct   61  NGFTYCVVAVDSAGREIPMAFLERVKEDFYKRYGGGKAATAAANSLNKEFGSNLKEHMQY  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLV  163
            C+DHP+E+S LAK KAQVSEVK +MMENIEKV RG    E+LV
Sbjct  121  CMDHPDEISNLAKAKAQVSEVKSLMMENIEKVLARGVICEMLV  163


>gb|AAB80624.1|  Strong similarity to Arabidopsis ATHSAR1 (gb|M90418). ESTs gb|T4
come from this gene. [Arabidopsis
thaliana]
Length=175

  Score =  260 bits (665),  Expect = 4e-68, Method: Compositional matrix adjust.
  Identities = 137/157 (87%), Positives = 150/157 (95%), Gaps = 0/157 (0%)

Query   63  FTYCVVAVESVGQQIPIAPMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
            F+YCVVAV+S G+QIP++F++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQYC+
Sbjct   19  FSYCVVAVDSAGRQIPMSFLERVKEDFNKRYGGGKAATAAANSLNKEFGSKLKEHMQYCM   78

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
            DHP+E+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR  GT
Sbjct   79  DHPDEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRTTGTQ  138

Query  183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            +RRKMWLQNMKIKLIVL IIALILII+LSVCHGFKC
Sbjct  139  MRRKMWLQNMKIKLIVLAIIIALILIIVLSVCHGFKC  175


>ref|XP_001764415.1|  [G]  R-SNARE, VAMP72-family [Physcomitrella patens subsp. pate
  gb|EDQ70682.1|  [G]  R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]
Length=238

  Score =  260 bits (665),  Expect = 5e-68, Method: Compositional matrix adjust.
  Identities = 120/220 (54%), Positives = 173/220 (78%), Gaps = 0/220 (0%)

Query    1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            MG   LIY+FVARGT +LAE+   + GNFSQIAVQCLLKLPAGTSKQTYVMDRHTFNFFVE
Sbjct    1  MGDARLIYSFVARGTTVLAEHAIYAGNFSQIAVQCLLKLPAGTSKQTYVMDRHTFNFFVE   60

Query   61  DGFTYCVVAVESVGQQIPIAPMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            +GFT+ VVA E++G+ IP AF++RVK+DF    Y GG+A  A ++SL+ EFG KLKEHM +
Sbjct   61  NGFFTLVVAEEALGRLIPFAFLERVKDDFKHHYQGGRADLAVSHSLDAEFGPKLKEHMDF  120

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+++PEE+ K++++K+QV+EVKG+MMENI+KVLDR +KI+LLVD+T +L+S A ++++ G
Sbjct  121  CMENPEEIKKISRIKSQVAEVKGIMMENIDKVLDRGDKIDLLSATTHLQSSAAEYQRAG  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH  220
            +RR++W Q+ ++KL+VL +I+ +  II LS+C GF CH
Sbjct  181  RVIRRRLWWQHFRLKLLVLLLIVVVAFIIYLSICRGFICH  220
```

```
>gb|EAZ39281.1| hypothetical protein OsJ_022764 [Oryza sativa (japonica cultivar
Length=273

 Score =  253 bits (646),  Expect = 6e-66, Method: Compositional matrix adjust.
 Identities = 136/248 (54%), Positives = 176/248 (70%), Gaps = 34/248 (13%)

Query    6  LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNN---------KFTYNCDGHTFN    56
            LIYAFVARGT +LAEYTEFTGNF  +A+QCL +LPAS         +F+Y CDGHTFN
Sbjct   23  LIYAFVARGTAVLAEYTEFTGNFPALAAQCLQRLPASGGGSGGGAPARFSYACDGHTFN    82

Query   57  YLVEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKE   116
            +L+  G+ YCVVA ESV + ++AF++R+K+DF KRYGGGKA TA A SLN+E+G  +K+
Sbjct   83  FLLHRGYAYCVVAKESVPKNVSVAFLERLKDDFMKRYGGGKADTALAKSLNKEYGPVIKQ   142

Query  117  HMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKV----------------------   152
            HMQY +DH EE+ K  KV+AQVSEVK +M+ENIEKV
Sbjct  143  HMQYVLDHSEEIEKTLKVQAQVSEVKNIMLENIEKVWSTFAVGCPLFFTELILMGFLPKK   202

Query  153  -LDRGEKIELLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIIL   211
             L RGEK+  L DKT +L+SQAQ+F+++G  +RRK WLQNMKIKL +VLGI++ L++I+ +
Sbjct  203  TLGRGEKLSELQDKTSDLQSQAQEFKKKGVKIRRKTWLQNMKIKLVLVLGILLLLVIIVWV   262

Query  212  SVCHGFKC   219
            SVC GF C
Sbjct  263  SVCQGFDC   270


>gb|EAZ25708.1| hypothetical protein OsJ_009191 [Oryza sativa (japonica cultivar
Length=183

 Score =  252 bits (644),  Expect = 1e-65, Method: Compositional matrix adjust.
 Identities = 123/217 (56%), Positives = 149/217 (68%), Gaps = 40/217 (18%)

Query    3  QQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDG    62
            + +L+Y+FVARG V+L
Sbjct    6  RTTLVYSFVARGAVVLGRPRR---------------------------------------    26

Query   63  FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV   122
            +YCVVA ES G+Q+P+ F++RVKEDF+K+Y GGKA A ANSL RE+G KLKEHM+YC
Sbjct   27  -AYCVVATESAGRQLPVGFIERVKEDFSKKYSGGKANATANSLKREYGPKLKEHMKYCD    85

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN   182
            DHPEE+  KLAKVKAQV+EVKGVMM+NIEKVLDRGEKIELLVDKTE+LRSQAQDF++ GT
Sbjct   86  AHPEEIDKLAKVKAQVTEVKGVMMQNIEKVLDRGEKIELLVDKTEDLRSQAQDFRKAGTK   145

Query  183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   219
            +RRKMW +NMK+KLIV GI++ALIL+II+VC
Sbjct  146  IRRKMWWENMKMKLIVFGIVVALILVIILTVCRDLNC   182


>ref|XP_001418265.1| ▯G▯ predicted protein [Ostreococcus lucimarinus CCE9901]
 gb|ABO96558.1| ▯G▯ predicted protein [Ostreococcus lucimarinus CCE9901]
Length=215

 GENE ID: 5002283 OSTLU_32248 | predicted protein
[Ostreococcus lucimarinus CCE9901] (10 or fewer PubMed links)

 Score =  246 bits (629),  Expect = 6e-64, Method: Compositional matrix adjust.
 Identities = 118/214 (55%), Positives = 160/214 (74%), Gaps = 2/214 (0%)

Query    6  LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY    65
            LIYAFVAR T +LAE+T ++GNF+TIA Q L KL   N +FTY  DGHTFNY +E+G  TY
Sbjct    3  LIYAFVARRTTVLAEFTNYSGNFSTIAIQALEKLSDDNTRFTYTADGHTFNYVVENGFTY    62

Query   66  CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP   125
            VVA   +G+ +P A +DR+K +FT+ +    +A A +SLN+ F  LKEH+++C  +P
Sbjct   63  LVVADSELGRHVPFACLDRIKSEFTRDHAS-EAQDAIAHSLNKSFAPRLKEHLEFCSANP   121

Query  126  EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR   185
            E VSK++ V+ QVS+VK +MM+NIEKVLDRGEKIELLVDK++ LR +A +F + G  +RR
Sbjct  122  EAVSKVSAVQQQVSQVKEIMMDNIEKVLDRGEKIELLVDKSDALRFEAANFHKTGRALRR   181

Query  186  KMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC   219
            +W QNMKIK+    II AL+L +I ++C G KC
```

```
Sbjct  182  NLWCQNMKIKVAFGLIIFALLLTLIFTLC-GKKC  214
```

>ref|**XP_001777794.1**| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. pate
  gb|**EDQ57456.1**| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]
Length=235

 Score = 244 bits (622), Expect = 4e-63, Method: Compositional matrix adjust.
 Identities = 121/218 (55%), Positives = 157/218 (72%), Gaps = 0/218 (0%)

```
Query    3  QQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDG   62
            ++ LIY+FV+RGT +LAEY  +GN   IA+QCL KLP  NNK TY CD HTFN+LVEDG
Sbjct    2  EEGLIYSFVSRGTTVLAEYASVSGNSNRIAAQCLAKLPGGNNKHTYVCDRHTFNFLVEDG   61

Query   63  FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
            FT+ VA E  +QI AF+DRVK DF  RY GG+A A   SLN EFG +LKEHM +
Sbjct   62  FTFLAVADEDFSRQIAFAFLDRVKNDFQHRYGGGRADLAVTYSLNAEFGPRLKEHMDFVA  121

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
            +PEE+ K++K+K+QV+EVK +MM NIEK+LDR E+I  LS A  F +QG
Sbjct  122  ANPEEIKKMSKIKSQVAEVKEIMMVNIEKLLDRNERIDLLVGKTDDLHSNAHVFEKQGNQ  181

Query  183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH  220
            +RR+ W + K+KL+VL +II +  II LS+C  F CH
Sbjct  182  IRRRAWCAHFKLKLLVLVLIIIVAFIIYLSICRDFICH  219
```

>ref|**NP_001067392.1**| **UG** Os12g0639800 [Oryza sativa (japonica cultivar-group)]
  gb|**ABA99617.1**| **G** Synaptobrevin family protein, expressed [Oryza sativa (japonic
cultivar-group)]
  dbj|**BAF30411.1**| **G** Os12g0639800 [Oryza sativa (japonica cultivar-group)]
Length=179

 GENE ID: 4352920 Os12g0639800 | Os12g0639800 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score = 236 bits (602), Expect = 9e-61, Method: Compositional matrix adjust.
 Identities = 133/219 (60%), Positives = 152/219 (69%), Gaps = 40/219 (18%)

```
Query    1  MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVE   60
            M +  LIYA VARGTV+LAE+T +GNF  IA+QCL KLP  NN  TY CD HTFN LIH
Sbjct    1  MAESKLIYAMVARGTVVLAEHTAYAGNFRDIAAQCLQKLPAGDNRLTYTCDAHTFNFLIH   60

Query   61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            G+ YCVVA ES G+QIP+A +D +KEDF KR                  +L E M+Y
Sbjct   61  QGYAYCVVATESSGRQIPLALLDMIKEDFNKR-----------------PRLGEQMKY   101

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
            C+DHPEEVSKLAKVKAQVSEVKG+MMENI+K             A DFRQQG
Sbjct  102  CMDHPEEVSKLAKVKAQVSEVKGIMMENIDK-----------------AADFRQQG     140

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC  219
            T VRRKMW QNMKIKLIVLGIIIALILIIILSVCHGFKC
Sbjct  141  TRVRRKMWYQNMKIKLIVLGIIIALILIIILSVCHGFKC  179
```

>ref|**XP_001692208.1**| **UG** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt
  gb|**EDP04158.1**| **G** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]
Length=218

 GENE ID: 5717896 VAMP71 | R-SNARE protein, VAMP72-family
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

 Score = 217 bits (552), Expect = 6e-55, Method: Compositional matrix adjust.
 Identities = 107/209 (51%), Positives = 143/209 (68%), Gaps = 1/209 (0%)

```
Query    6  LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY   65
            LIY+ V++GTV LAEY +GNF  A   L  K   + KFT+N DGHTFN+L   GFTY
Sbjct    3  LIYSSVSQGTVTLAEYAAFSGNFGAVAKDYLEKAGKNEGKFTFNVDGHTFNLNRGGFTY   62

Query   66  CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP  125
```

```
              VVA E+ G+ IP AF+D++  +F  ++    KAA A    LN  FG +LK  M++    +P
Sbjct  63     LVVADEAYGRAIPSAFLDKMASEFAMKFAD-KAAGAKEGGLNGSFGKQLKSMMEHATQYP   121

Query  126    EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR   185
              EE SK+A V+ +V EVKG+M ENIEKVL RGEK+ELL DKTENL ++A  F++ G  +RR
Sbjct  122    EEYSKVASVQKKVDEVKGIMTENIEKVLARGEKLELLTDKTENLMNEADRFQRTGRTLRR   181

Query  186    KMWLQNMKIKLIVLGIIIALILIIILSVC   214
              KMW  QN K+K++V   +I L ++I L VC
Sbjct  182    KMWWQNCKMKIVVALAVILLAVVIFLLVC   210
```

>gb|EAZ03380.1| hypothetical protein OsI_024612 [Oryza sativa (indica cultivar-g
Length=322

                                          Sort alignments for this
                                            E value   Score   Percen
                                                 Query start position

 Score = 201 bits (511), Expect = 3e-50, Method: Compositional matrix adjust.
 Identities = 96/156 (61%), Positives = 121/156 (77%), Gaps = 9/156 (5%)

```
Query  6      LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNN---------KFTYNCDGHTFN   56
              LIYAFVARGT +LAEYTEFTGN+ +A+QCL +LPAS       +F+Y CDGHTFN
Sbjct  23     LIYAFVARGTAVLAEYTEFTGNFPALAAQCLQRLPASGGGGSGGGAPARFSYACDGHTFN   82

Query  57     YLVEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKE   116
              +L+  G+ YCVVA ESV + + +AF++R+K+DF KRYGGGKA TA A SLN+E+G +VK+
Sbjct  83     FLLHRGYAYCVVAKESVPKNVSVAFLERLKDDFMKRYGGGKADTALAKSLNKEYGPVIKQ   142

Query  117    HMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKV   152
              HMQY +DH EE+ K  KV+AQVSEVK +M+ENIEKV
Sbjct  143    HMQYVLDHSEEIEKTLKVQAQVSEVKNIMLENIEKV   178
```

 Score = 70.9 bits (172), Expect = 5e-11, Method: Compositional matrix adjust.
 Identities = 40/69 (57%), Positives = 56/69 (81%), Gaps = 0/69 (0%)

```
Query  151    KVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIII   210
              + L RGEK+   L DKT +L+SQAQ+F+++G  +RRK WLQNMKIKL+VLGI++ L++I+
Sbjct  251    QTLGRGEKLSELQDKTSDLQSQAQEFKKKGVKIRRKTWLQNMKIKLVVLGILLLLVIIVW   310

Query  211    LSVCHGFKC   219
              +SVC GF C
Sbjct  311    VSVCQGFDC   319
```

>ref|XP_001692312.1| [UG] R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt
 gb|EDP04262.1| [G] R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]
Length=219

GENE ID: 5717794 VAMP74 | R-SNARE protein, VAMP72-family
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

 Score = 186 bits (472), Expect = 9e-46, Method: Compositional matrix adjust.
 Identities = 93/209 (44%), Positives = 129/209 (61%), Gaps = 0/209 (0%)

```
Query  6      LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY   65
              L+Y  V +G+V LAEY  F GNF +A   L K     K  Y  DGH+ N+L  GFTY
Sbjct  3      LVYVSVCQGSVALAEYAGFQGNFAVVARDYLDKATKLEGKSRYEVDGHSLNFLNRGGFTY   62

Query  66     CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP   125
              V+A    G  +P AF+D+V+ +F  +YG G    AAA SLN FG +LK+  +   HP
Sbjct  63     LVIASVDSGVALPSAFLDKVEAEFRAKYGAGLQLGAANGSLNATFGKQLQLTENATQHP   122

Query  126    EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR   185
              EE SK+A V+ +V E K VM++NI+ VL RGEK+E + +KTE+L ++A  FR    V+R
Sbjct  123    EEFSKVAAVQKKVDEAKAVMVDNIDAVLRGKELKELQIQEKTEDLMAEADRFRDGAVRVKR   182

Query  186    KMWLQNMKIKLIVLGIIIALILIIILSVC   214
              K+W QN K+K++V   +I L ++I L VC
Sbjct  183    KLWWQNCKMKIVVALAVILLAVVIFLLVC   211
```

>emb|CAL53602.1| SYNAPTOBREVIN-RELATED PROTEIN 1 (IC) [Ostreococcus tauri]
Length=185

 Score = 182 bits (462), Expect = 1e-44, Method: Compositional matrix adjust.
 Identities = 94/184 (51%), Positives = 138/184 (75%), Gaps = 2/184 (1%)

```
Query  36   LMKLPASNNKFTYNCDGHTFNYLVEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGG  95
            L K+  +FTY  DGHTFNY+VE+GFTY VVA  S G+ +P A +DR+K +F + +
Sbjct  2    LEKISEDNTRFTYTADGHTFNYVVENGFTYLVVADSSGRHVPFACLDRIKAEFARDHAS   61

Query  96   GKAATAAANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDR  155
            +A A A+SLN+ F +LKEH++C +PE VSK+++V+ QVS+VK +MM+NIEKVLDR
Sbjct  62   -EAQDAIAHSLNKSFAPRLKEHLEFCSANPEAVSKVSQVQQQVSQVKEIMMDNIEKVLDR  120

Query  156  GEKIELLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCH  215
            GEKIE+LVDK++ LR QA +F + G +RR+MW +NMK+K++V  I++A++  +I ++C
Sbjct  121  GEKIEILVDKSDALRFQADNFHKTGRQLRRRMWCENMKMKVLVGVIVLAILFTLIFTLC-  179

Query  216  GFKC  219
            G KC
Sbjct  180  GKKC  183
```

>ref|XP_001692324.1| **UG** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt
 gb|EDP04274.1| **G** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]
Length=220

 GENE ID: 5717908 VAMP73 | R-SNARE protein, VAMP72-family
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

 Score = 182 bits (462), Expect = 1e-44, Method: Compositional matrix adjust.
 Identities = 91/200 (45%), Positives = 125/200 (62%), Gaps = 2/200 (1%)

```
Query  16   VILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTYCVVAVESVGQ  75
            V LAEY F GNF +A + L +    K +Y DGHTF L  GF + V A E G+
Sbjct  14   VTLAEYAAFAGNFGAVAKEYLAR-TTGEGKLSVADVDGHTFTVLCRGGFVFLVAADEATGK  72

Query  76   QIPIAFMDRVKEDFTKRYGGGKAATAAA-NSLNREFGSKLKEHMQYCVDHPEEVSKLAKV  134
            IP AF+D+V ++FT +Y   A A   L FG +LK  M++   +PEE SK+A V
Sbjct  73   TIPSAFVDKVADEFTSKYADKAAGLAGKEGGLQSSFGKQLKSTMEHATQYPEEYSKVASV  132

Query  135  KAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKI  194
            + +V EVKG+M ENI+KVL RGEK+ELL DKTENL  ++  F + G +RR+MW+QN K+
Sbjct  133  QKKVDEVKGIMTENIDKVLARGEKLELLTDKTENLMFESDRFVRTGRALRRRMWMQNCKM  192

Query  195  KLIVLGIIIALILIIILSVC  214
            K++V   +I L ++I L VC
Sbjct  193  KIVVALAVILLAVVIFLLVC  212
```

>ref|NP_196676.1| **UG** ATVAMP713 (Arabidopsis thaliana vesicle-associated membran
713)
 sp|Q9LFP1|VA713_ARATH **G** Vesicle-associated membrane protein 713 (AtVAMP713)
 emb|CAB96650.1| **G** putative protein [Arabidopsis thaliana]
 gb|AAM14024.1| **G** unknown protein [Arabidopsis thaliana]
 gb|AAM67467.1| **G** unknown protein [Arabidopsis thaliana]
Length=221

 GENE ID: 830984 ATVAMP713 | ATVAMP713 (Arabidopsis thaliana vesicle-associated
membrane protein 713) [Arabidopsis thaliana] (10 or fewer PubMed links)

 Score = 167 bits (424), Expect = 4e-40, Method: Compositional matrix adjust.
 Identities = 86/215 (40%), Positives = 141/215 (65%), Gaps = 6/215 (2%)

```
Query  5    SLIYAVARGTVILAEYTEFTGNFTTIASQCLMKLPA--SNNKFTYNCDGHTFNYLVEDG  62
            ++I+A VARGTV+L+E++ + N ++I+ Q L KLP  S++  +Y+ D + F+    DG
Sbjct  2    AIIFALVARGTVVLSEFSATSTNASSISKQILEKLPGNDSDSHMSYSQDRYIFHVKRTDG  61

Query  63   FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
            T    +A E+ G+ IP AF+D + + F K YG    +A A S+N EF   L + M++
Sbjct  62   LTVLCMADETAGRNIPFAFLDDIHQRFVKTYGRA-IHSAQAYSMNDEFSRVLSQQMEFYS  120
```

```
Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
            + P    +++++K ++S+V+ VM+ENI+KVLDRGE++ELLVDKTEN++     FR+Q
Sbjct  121  NDPN-ADRMSRIKGEMSQVRNVMIENIDKVLDRGERLELLVDKTENMQGNTFRFRKQARR  179

Query  183  VRRKMWLQNMKIKLIVLGIIIALILIIILS-VCHG  216
            R  MW +N+K+  I L +++AL++  I ++ VCHG
Sbjct  180  YRTIMWWRNVKLT-IALILVLALVVYIAMAFVCHG  213


>ref|NP_197628.1| UG ATVAMP714 (Vesicle-associated membrane protein 714) [Arabi
thaliana]
  sp|Q9FMR5|VA714_ARATH G Vesicle-associated membrane protein 714 (AtVAMP714)
  dbj|BAB08335.1| G synaptobrevin-like protein [Arabidopsis thaliana]
Length=221

  GENE ID: 832297 ATVAMP714 | ATVAMP714 (Vesicle-associated membrane protein 714)
[Arabidopsis thaliana] (10 or fewer PubMed links)

  Score = 161 bits (408),  Expect = 2e-38, Method: Compositional matrix adjust.
  Identities = 79/214 (36%), Positives = 137/214 (64%), Gaps = 4/214 (1%)

Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPA--SNNKFTYNCDGHTFNYLVEDG  62
            +++YA VARGT+VLAE++  TGN  + + L KL   S+ ++ D + F+ L  DG
Sbjct    2  AIVYAVVARGTVVLAEFSAVTGNTGAVVRRILEKLSPEISDERLCFSQDRYIFHILRSDG  61

Query   63  FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
            T+  +A ++ G+++P ++++   F  K YG   A A  ++N EF   L + M++
Sbjct   62  LTFLCMANDTFGRRVPFSYLEEIHMRFMKNYGK-VAHNAPAYAMNDEFSRVLHQQMEFFS  120

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
            +P  V  L +V+ +VSE++ VM+ENIEK+++RG++IELLVDKT  ++   FR+Q
Sbjct  121  SNPS-VDTLNRVRGEVSEIRSVMVENIEKIMERGDRIELLVDKTATMQDSSFHFRKQSKR  179

Query  183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHG  216
            +RR +W++N K+ +++ +I+ L+ III S C G
Sbjct  180  LRRALWMKNAKLLVLLTCLIVFLLYIIIASFCGG  213


>gb|ABM30199.2| synaptobrevin-like protein [Brassica juncea]
Length=221

  Score = 161 bits (408),  Expect = 3e-38, Method: Compositional matrix adjust.
  Identities = 79/214 (36%), Positives = 138/214 (64%), Gaps = 4/214 (1%)

Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPA--SNNKFTYNCDGHTFNYLVEDG  62
            ++IYA VARGT+VLAE++  TGN   + + L KL   S+  ++ D + F+ L  DG
Sbjct    2  AIIYAVVARGTVVLAEFSAVTGNTDAVVRRILEKLSPETADERLCFSQDRYIFHILRSDG  61

Query   63  FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
            T+  +A ++ G+++P ++++   F  K YG   A A  ++N EF   L + M++
Sbjct   62  LTFLCMANDTFGRRIPFSYLEEIQMRFMKNYGK-VAHQAPAYAMNDEFSRVLHQQMEFFS  120

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
            +P  V  L +V+ +VSE++ VM+ENIEK+++RG++IELLVDKT   A  FR+Q
Sbjct  121  SNPS-VDTLNRVRGEVSEIRSVMVENIEKIMERGDRIELLVDKTATMQDSAFHFRKQSKR  179

Query  183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHG  216
            +RR +W++N K+ +++ +I+ L+ III S C G
Sbjct  180  LRRALWMKNAKLLVMLTCVIVLVLYIIIASFCGG  213


>pir||B71423  hypothetical protein - Arabidopsis thaliana]
  emb|CAB10356.1| SYBL1 like protein [Arabidopsis thaliana]
  emb|CAB78620.1| SYBL1 like protein [Arabidopsis thaliana]
Length=159

  Score = 160 bits (405),  Expect = 5e-38, Method: Compositional matrix adjust.
  Identities = 82/146 (56%), Positives = 98/146 (67%), Gaps = 35/146 (23%)

Query    1  MGGQSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLP-ASNNKFTYNCDGHTFNYLV  59
            MGG+S IY+FVARGT+ILAEYTEFTGNF +IA+QCL KLP +SN+KFTYNCD HTFN+LV
Sbjct    1  MGGESFIYSFVARGTMILAEYTEFTGNFPSIAAQCLQKLPSSSNSKFTYNCDHHTFNFLV  60
```

```
Query  60  EDG--------------------------------FTYCVVAVESVGQQIPIAFMDRV  85
               ED                                    + YCVVA +S+ +QI IAF++RV
Sbjct  61  EDAYGWSLSLSSSLETNNLYLLWFGDETTHMCFKIICYAYCVVAKDSLSKQISIAFLERV  120

Query  86  KEDFTKRYGGGKAATAAANSLNREFG  111
               K DF KRYGGGKA+TA A SLN+EFG
Sbjct  121 KADFKKKRYGGGKASTAIAKSLNKEFG  146
```

>ref|NP_194942.1| **UG** VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C) [Arabidops thaliana]

  sp|O49377|VA711_ARATH **G** Vesicle-associated membrane protein 711 (AtVAMP711) (v-synaptobrevin 7C) (AtVAMP7C)

  gb|AAL27509.1|AF439840_1 **G** AT4g32150/F10N7_40 [Arabidopsis thaliana]
  6 more sequence titles

emb|CAA16574.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]

  gb|AAD01748.1| **G** vesicle-associated membrane protein 7C; synaptobrevin 7C [Arab thaliana]

  emb|CAB79933.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]

  gb|AAM65673.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]

  gb|AAM78063.1| **G** AT4g32150/F10N7_40 [Arabidopsis thaliana]

  dbj|BAE98551.1| **G** vesicle-associated membrane protein 7C [Arabidopsis thaliana]
Length=219

  GENE ID: 829347 VAMP7C | VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C)
[Arabidopsis thaliana] (10 or fewer PubMed links)

 Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.
 Identities = 80/213 (37%), Positives = 137/213 (64%), Gaps = 3/213 (1%)

```
Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNK-FTYNCDGHTFNYLVEDGF   63
            +++YA VARGTV+L+E+T  + N +TIA Q L K+P  N+   +Y+ D + F+   DG
Sbjct    2  AILYALVARGTVVLSEFTATSTNASTIAKQILEKVPGDNDSNVSYSQDRYVFHVKRTDGL   61

Query   64  TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
            T   +A E+ G++IP AF++ + F + YG      TA A ++N EF    L + + Y +
Sbjct   62  TVLCMAEETAGRRIPFAFLEDIHQRFVRTYGRA-VHTALAYAMNEEFSRVLSQQIDYYSN  120

Query  124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
              P    ++ ++K ++++V+GVM+ENI+KVLDRGE++ELLVDKT N++      FR+Q
Sbjct  121  DPN-ADRINRIKGEMNQVRGVMIENIDKVLDRGERLELLVDKTANMQGNTFRFRKQARRF  179

Query  184  RRKMWLQNMKIKLIVLGIIIALILIIILSVCHG  216
            R   +W +N K+ ++++ +++ +I I +  +CHG
Sbjct  180  RSNVWWRNCKLTVLLILLLLVIIYIAVAFLCHG  212
```

>emb|CAO44255.1| unnamed protein product [Vitis vinifera]
Length=220

 Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.
 Identities = 73/214 (34%), Positives = 135/214 (63%), Gaps = 3/214 (1%)

```
Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNK-FTYNCDGHTFNYLVEDGF   63
            +++YA VARG+++LAE++  + N + IA Q L K+P  N+   +Y+ D RY F+   DG
Sbjct    2  TILYALVARGSLVLAEFSGTSTNASAIARQILEKIPGDNDSNVSYSQDRYIFHVKRTDGL   61

Query   64  TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
            T   +A ++ G++IP AF++ + + + F + YG     +A A  +N +F   L + M+Y +
Sbjct   62  TVLCMADDTAGRRIPFAFLEDIHQRFVRTYGRA-VHSAQAYAMNDDFSRVLSQQMEYYSN  120

Query  124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
              P    ++ ++K ++  +V+ VM+ENI+KVLDRG+++ELLVDKT N++      FR+Q
Sbjct  121  DPN-ADRINRLKGEMGQVRNVMIENIDKVLDRGDRLELLVDKTANMQGNTFRFRKQARRF  179

Query  184  RRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
            R   +W +N+K+ +  ++ I++ ++ ++I+   CHG
```

```
Sbjct  180  RSTVWWRNVKLTVALIIILLVIVYVILAFACHGL  213
```

>ref|XP_001762112.1| **UG** R-SNARE, VAMP71-family [Physcomitrella patens subsp. pa

  gb|EDQ73216.1| **G** R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]
Length=220

 Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.
 Identities = 77/191 (40%), Positives = 128/191 (67%), Gaps = 3/191 (1%)

```
Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLP-ASNNKFTYNCDGHTFNYLVEDGF   63
            +++YA VARGTV+LAE++  +GN +TIA + L KLP    +++ +Y+ D H F+ L  DG
Sbjct    2  AILYALVARGTVVLAEFSAASGNASTIARRILEKLPPGGDSRVSYSQDRHIFHILKADGL   61

Query   64  TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
            T+  +A +S G++IP A+++ +   FK YG  A+TA A ++N EF  L + M+Y
Sbjct   62  TFLCMATDSFGRRIPFAYLEDIHMRFMKNYGK-VASTALAYTMNDEFSRVLHQQMEYFST  120

Query  124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
            + ++  + +VK ++ EV+ VM+ENI+KVL+RG++IELLVDKT  ++    F++Q  +
Sbjct  121  N-KQADSINRVKGEIVEVRAVMVENIDKVLERGDRIELLVDKTDNTFRFKKQSRRL       179

Query  184  RRKMWLQNMKI  194
            R+ MW++N K+
Sbjct  180  RQAMWIKNAKL  190
```

>ref|NP_001064184.1| **UG** Os10g0154000 [Oryza sativa (japonica cultivar-group)]

  gb|ABB46773.2| **G** Synaptobrevin family protein, expressed [Oryza sativa (japonic
cultivar-group)]

  dbj|BAF26098.1| **G** Os10g0154000 [Oryza sativa (japonica cultivar-group)]
Length=226

 GENE ID: 4348130 Os10g0154000 | Os10g0154000 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.
 Identities = 79/221 (35%), Positives = 134/221 (60%), Gaps = 9/221 (4%)

```
Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPA-SNNKFTYNCDGHTFNYL-----   58
            +++YA VARGTV+LAE++  +GN  + L KLP  + ++ +Y+ D H F+     
Sbjct    2  AIVYAVVARGTVVLAEFSAVSGNAGAVARRILEKLPPDAESRLCFAQDRYIFHVLRSPPP   61

Query   59  -VEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEH  117
                DG T+  +A ++ G++IP  +++  F K YG   A A ++N EF   L +
Sbjct   62  AAADGLTFLCMANDTFGRRIPFLYLEDIQMRFIKNYGR-IAHNALAYAMNDEFSRVLHQQ  120

Query  118  MQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR  177
            M+Y   +P    L +++ +VSE+  VM++NIEK+LDRGE+I LLVDKT   + A FR
Sbjct  121  MEYFSSNPS-ADTLNRLRGEVSEIHTVMVDNIEKILDRGERISLLVDKTSTMQDSAFHFR  179

Query  178  QQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFK   218
            +Q  +RR +W++N K+  ++  +I+ L+ +II + C G
Sbjct  180  KQSRRLRRALWMKNAKLLAVLTAVIVLLLYLIIAAFCGGLS  220
```

>ref|XP_001778044.1| **UG** R-SNARE, VAMP71-family [Physcomitrella patens subsp. pa

  gb|EDQ57153.1| **G** R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]
Length=220

 Score = 155 bits (392), Expect = 2e-36, Method: Compositional matrix adjust.
 Identities = 75/191 (39%), Positives = 128/191 (67%), Gaps = 3/191 (1%)

```
Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLP-ASNNKFTYNCDGHTFNYLVEDGF   63
            +++YA VARGTV+LAE++  +GN +TIA + L K+P    +++ +Y+ D H F+ +  DG
Sbjct    2  TILYALVARGTVLLAEFSAASGNGSTIARRILEKLPPGGDSRVSYSQDRHIFHIMKADGL   61

Query   64  TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
            T+  +A +S G++IP A+++ ++   F K YG  A+TA A ++N EF  L + M+Y
Sbjct   62  TFLCMASDSFGRRIPFSYLEDIHMRFMKNYGK-VASTALAYAMNDEFSRVLHQQMEYFSR  120
```

```
Query   124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
             +P       + +VK +++EV+ VM+ENI+KVL+RG++IELLVDKT  ++    F++Q   +
Sbjct   121  NPN-ADTINRVKGEIAEVRAVMVENIDKVLERGRDIELLVDKTSTIQDNTFRFKKQSRRL  179

Query   184  RRKMWLQNMKI  194
             R+ MW++N K+
Sbjct   180  RQAMWMKNAKL  190
```

>ref|XP_001631076.1| **G** predicted protein [Nematostella vectensis]

gb|EDO39013.1| **G** predicted protein [Nematostella vectensis]
Length=223

GENE ID: 5510622 NEMVEDRAFT_v1g209672 | predicted protein
[Nematostella vectensis] (10 or fewer PubMed links)

Score = 155 bits (391), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 72/212 (33%), Positives = 125/212 (58%), Gaps = 1/212 (0%)

```
Query   6    LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY  65
             ++Y+ V+RGT +LA+++    GNF  +  Q L ++P  N+K TY   + F+Y+ ED   Y
Sbjct   3    ILYSVVSRGTTVLAKFAACAGNFAEVTEQILSRIPPDNSKLTYTQGSYLFHYISEDRIIY  62

Query   66   CVVAVESVGGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP  125
             +  ++    +    ++  +K F  YG +A TA  ++F  L  M++ D
Sbjct   63   LCITDDAFERSQAFLYLTEIKRRFQAAYHG-RAQTALPFAMNSEFSRVLSAEMKHYSDSR  121

Query   126  EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR  185
             EE S +AKV+ ++ E++G+M++NI++  RGE++ELL+DK E+L S +  F++    + R
Sbjct   122  EEGSSIAKVQVELEDEIRGIMVKNIDSIASRGERLELLIDKAEDLNSSSLTFKKTSRGLAR  181

Query   186  KMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
             MW  +N+KI LI++ I I +I  I+ + C+G
Sbjct   182  AMWWKNVKITLILIAISIVVIYFIVSAACNGL  213
```

>ref|XP_001769494.1| **UG** R-SNARE, VAMP71-family [Physcomitrella patens subsp. pa

gb|EDQ65655.1| **G** R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]
Length=220

Score = 154 bits (389), Expect = 5e-36, Method: Compositional matrix adjust.
Identities = 73/191 (38%), Positives = 128/191 (67%), Gaps = 3/191 (1%)

```
Query   5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLP-ASNNKFTYNCDGHTFNYLVEDGF  63
             +++YA VARGTV+LAE++  +GN +TIA + L K+P  +++ +Y+ D H F+ +   DG
Sbjct   2    TILYALVARGTVVLAEFSAASGNSSTIARRILEKIPPGGDSRVSYSQDRHIFHIMKADGL  61

Query   64   TYCVVAVESVGGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
             T+ +A ++ G++IP ++  ++ +N EF  L  M+Y
Sbjct   62   TFLCMASDTFGRRIPFSYLEDIHMRFMKSYGK-VASTALAYAMNDEFSRVLHQQMEYFSS  120

Query   124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
             +P      + +VK +++EV+ VM+ENI+KVL+RG+++IELLVDKT  ++    F++Q   +
Sbjct   121  NPN-ADTINRVKGEIAEVRAVMVENIDKVLERGRDIELLVDKTSTIQDNTFRFKKQSRQL  179

Query   184  RRKMWLQNMKI  194
             ++ MW++N K+
Sbjct   180  KQAMWMKNAKL  190
```

>gb|ABK93000.1| unknown [Populus trichocarpa]
Length=220

Score = 150 bits (380), Expect = 4e-35, Method: Compositional matrix adjust.
Identities = 77/214 (35%), Positives = 137/214 (64%), Gaps = 3/214 (1%)

```
Query   5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNK-FTYNCDGHTFNYLVEDGF  63
             +++YA VARG+V+LAE+T    N + IA Q L K+P +++     +Y+ D + F+    DG
Sbjct   2    AILYALVARGSVVLAEFTSTATNASAIARQILDKIPNDDSNRVSYSQDRYIFHVKRTDGL  61

Query   64   TYCVVAVESVGGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
             T   +A E+ G++IP AF++ + + F + YG    TA A ++N EF  L + M+Y +
Sbjct   62   TVLCMADETAGRRIPFAFLEDIHQRFVRTYGRA-VITAQAYAMNDEFSRVLSQQMEYYTN  120
```

```
Query  124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
            P    ++K ++S+V+ VM+ENI+VK+L+RG+++ELLVDKT N++      FR+Q
Sbjct  121  DPN-ADRINRLKGEMSQVRNVMIENIDKVLERGDRLELLVDKTANMQGNTFRFRKQARRF  179

Query  184  RRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
            R   +W +N+K+ + ++ +++ +I.+++   VCHG
Sbjct  180  RSTVWWRNVKLTVALILLLLVIIYVVLAFVCHGL  213


>ref|XP_001698008.1| U G  R-SNARE protein, VAMP71-family [Chlamydomonas reinhardt
 gb|EDO99593.1| G  R-SNARE protein, VAMP71-family [Chlamydomonas reinhardtii]
Length=218

 GENE ID: 5723646 VAMP75 | R-SNARE protein, VAMP71-family
[Chlamydomonas reinhardtii] (10 or fewer PubMed links)

 Score =  150 bits (379),  Expect = 6e-35, Method: Compositional matrix adjust.
 Identities = 85/214 (39%), Positives = 124/214 (57%), Gaps = 5/214 (2%)

Query    4  QSLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGF  63
            Q.++++ VARG V+LAE  TGN   IA + L KLP  + +Y +   F+ +V DG
Sbjct    5  QKILFSLVARGQVVLAE-NRVTGNVNVIAVRILEKLPHEDTRVSYTQERFMFHVMVSDGI  63

Query   64  TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
            TY  VA E  G++IP AF+D V+   YG   A  A   N EF   L E   D
Sbjct   64  TYMAVAEFGRRIPFAFLDDVRGRFVAMYGVA-AKEAVAYEYNTEFSRVLAERAAHFSD  122

Query  124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
            +  + + +VK ++ EVK +M+ENIEKVL+RGE+++LLVDKTE L+ +   FR++ +
Sbjct  123  PSADA--INRVKGELQEVKHIMIENIEKVLERGERLDLLVDKTEGLQQVSLAFRREARRL  180

Query  184  RRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
            +  MW +N K+ ++V     LI I+  VC GF
Sbjct  181  KHTMWWKNAKLWVLVCAATALLIYFILGMVC-GF  213


>ref|XP_001745842.1| G  predicted protein [Monosiga brevicollis MX1]
 gb|EDQ89266.1| G  predicted protein [Monosiga brevicollis MX1]
Length=236

 Score =  149 bits (376),  Expect = 1e-34, Method: Compositional matrix adjust.
 Identities = 77/195 (39%), Positives = 119/195 (61%), Gaps = 4/195 (2%)

Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
            +LIYA VAR  ILAE+TE +GNFTT+   L K+P S+ + TY  + F+Y+
Sbjct    3  ALIYALVARDNTILAEFTENSGNFTTVTQSILDKIPNSDQRRTYVYDRYLFHYVREDGIV  62

Query   65  YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            Y  +A ES G++ P AF+++ ++DF     K++ A A  LNREF   LK  M
Sbjct   63  YLCLADESFGRRAPFAFLAQIMKDFKPYKSASKSSIAYA---LNREFAPVLKRMQMAFNKG  120

Query  125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            ++  L + ++   VK VM+ENIEKVL RGE+I+++V+K E+L  +++ F+    ++
Sbjct  121  SDDA--LDRARGEIEGVKHVMVENIEKVLQRGEQIDIMVEKAEDLSHESKRFQTSARKLK  178

Query  185  RKMWLQNMKIKLIVL  199
            +MW +N K  L++
Sbjct  179  NRMWWENQKFCLLLF  193


>ref|XP_001879548.1| G  VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H
 gb|EDR10163.1| G  VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H82]
Length=224

 Score =  148 bits (373),  Expect = 3e-34, Method: Compositional matrix adjust.
 Identities = 79/211 (37%), Positives = 132/211 (62%), Gaps = 8/211 (3%)

Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
            SLI+A VA+GT +LAE+       +F+     L K+P +N+K TY  + F+Y+ EDG+T
Sbjct    2  SLIHALVAKGTTVLAEHKAGGRDFSQATQTILSKIPPNNSKLTYAWEQYQFHYISEDGYT  61
```

```
Query   65  YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATA---AANSLNREFGSKLKEHMQ-Y  120
                Y V+A +SVG++   AF+  ++   FT        A SL    FG  +   +Q Y
Sbjct   62  YLVMADDSVGRRTSFAFLADLQRKFTAAPSSSSSSSQDEIPAYSLQGSFGPTISALLQTY  121

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
                P +  +LA+ +  ++++VK +M++N+E+     L  RGE+IELLVDKT +   QA  FR+
Sbjct  122  NTAPPSD--ELARAQNELNQVKDIMVQNVEQILSRGERIELLVDKTDVMAGQATAFRRGA  179

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIIL  211
                +VRR+MW +N   K+I L +++AL L+ +L
Sbjct  180  RSVRRQMWWKNS--KMIALSVVVALFLLWLL  208
```

>gb|BAY77730.1| hypothetical protein OsI_031689 [Oryza sativa (indica cultivar-g
Length=223

 Score = 146 bits (369), Expect = 9e-34, Method: Compositional matrix adjust.
 Identities = 77/221 (34%), Positives = 131/221 (59%), Gaps = 12/221 (5%)

```
Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPA-SNNKFTYNCDGHTFNYL-----  58
                +++YA VARGTV+LAE++   +GN   +A + L KLP  + ++   + D + F+ L
Sbjct    2  AIVYAVVARGTVVLAEFSAVSGNAGAVARRILEKLPPDAESRLCFAQDRYIFHVLRSPPP  61

Query   59  -VEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEH  117
                DG T+  +A ++ G++IP  +++  ++   F K YG   A  A  ++N EF     L +
Sbjct   62  TAADGLTFLCMANDTFGRRIPFLYLEDIQMRFIKNYGR-IAHNLALAYAMNDEFSRVLHQQ  120

Query  118  MQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR  177
                M+Y   +P    L +++    E+   VM++NIEK+LDRGE+I LLVDKT   ++A  FR
Sbjct  121  MEYFSSNPS-ADTLNRLRG---EIHTVMVDNIEKILDRGERISLLVDKTSTMQDSAFHFR  176

Query  178  QQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFK  218
                +Q    +RR +W++N K+  ++   +I+ L+ +II + C G
Sbjct  177  KQSRRLRRALWMKNAKLLAVLTAVIVLLLYLIIAAFCGGLS  217
```

>gb|AAM14694.1|AC097446_23 Putative synaptobrevin-like protein [Oryza sativa (ja
 gb|EAZ15333.1| hypothetical protein OsJ_029542 [Oryza sativa (japonica cultivar
Length=223

 Score = 146 bits (369), Expect = 9e-34, Method: Compositional matrix adjust.
 Identities = 77/221 (34%), Positives = 131/221 (59%), Gaps = 12/221 (5%)

```
Query    5  SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPA-SNNKFTYNCDGHTFNYL-----  58
                +++YA VARGTV+LAE++   +GN   +A + L KLP  + ++   + D + F+ L
Sbjct    2  AIVYAVVARGTVVLAEFSAVSGNAGAVARRILEKLPPDAESRLCFAQDRYIFHVLRSPPP  61

Query   59  -VEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEH  117
                DG T+  +A ++ G++IP  +++  ++   F K YG   A  A  ++N EF     L +
Sbjct   62  AAADGLTFLCMANDTFGRRIPFLYLEDIQMRFIKNYGR-IAHNLALAYAMNDEFSRVLHQQ  120

Query  118  MQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFR  177
                M+Y   +P    L +++    E+   VM++NIEK+LDRGE+I LLVDKT   ++A  FR
Sbjct  121  MEYFSSNPS-ADTLNRLRG---EIHTVMVDNIEKILDRGERISLLVDKTSTMQDSAFHFR  176

Query  178  QQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFK  218
                +Q    +RR +W++N K+  ++   +I+ L+ +II + C G
Sbjct  177  KQSRRLRRALWMKNAKLLAVLTAVIVLLLYLIIAAFCGGLS  217
```

>ref|XP_642704.1| U G synaptobrevin domain-containing protein [Dictyostelium dis
AX4]
 sp|Q86AQ7.1|VAM7B_DICDI Vesicle-associated membrane protein 7B
 gb|AA051196.1| similar to Arabidopsis thaliana (Mouse-ear cress). Synaptobrevin
protein [Dictyostelium discoideum]
 gb|EAL68772.1| G synaptobrevin domain-containing protein [Dictyostelium discoid
AX4]
Length=260

 GENE ID: 3393839 vamp7B | longin domain-containing protein
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

 Score = 146 bits (368), Expect = 1e-33, Method: Compositional matrix adjust.

```
   Identities = 79/214 (36%), Positives = 132/214 (61%), Gaps = 3/214 (1%)

Query   6   LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY   65
            +IY+ VARG+ +LAE+T   GNF TI   + L  +P ++ K +Y + + F+YLV D  TY
Sbjct   3   IIYSLVARGSSVLAEFTSTNGNFVTTTRRILDLIPPNDTKMSYVYEKYIFHYLVSDTLTY   62

Query  66   CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP  125
            +AE G++IP F+D VK F  Y G K  TA A  +N +F  L+  M +     +
Sbjct  63   LCMADEEFGRRIPFTFLDDVKNRFKSMY-GDKGKTAIAYGMNSDFSRTLENLDHH-YSNT  120

Query 126   EEVSKLAKVKAQVSEVKGVMMENI-EKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
            V   +++  A++ EVK +++ +I   +L RGEKIE+LV++T+ L  Q+  F++Q     ++
Sbjct 121   TRVDTMSRTMAEIDEVKNILVSDIAPQLLKRGEKIEMLVERTDTLNQQSFKFKKQSKQLK  180

Query 185   RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFK  218
            MW +N+K+ L++ I++ +I II++S C GF+
Sbjct 181   CAMWWKNVKLMLVLGAIVLIIIFIIVMSYCDGFR  214


>ref|NP_001056946.1|  UG Os06g0174400 [Oryza sativa (japonica cultivar-group)]
 dbj|BAA95814.1|  G putative synaptobrevin 1 [Oryza sativa Japonica Group]
 dbj|BAF18860.1|  G Os06g0174400 [Oryza sativa (japonica cultivar-group)]
Length=221

  GENE ID: 4340278 Os06g0174400 | Os06g0174400 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score = 145 bits (367),  Expect = 1e-33, Method: Compositional matrix adjust.
 Identities = 72/215 (33%), Positives = 133/215 (61%), Gaps = 4/215 (1%)

Query   5   SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPA--SNNKFTYNCDGHTFNYLVEDG   62
            +++YA VARGTV+LAE++    N   +A Q L +LP    +++  +Y  D + F+   DG
Sbjct   2   AILYAVVARGTVVLAEHSAAATNAGAVARQVLERLPGGDSHVSYTQDRYVFHAKRTDG   61

Query  63   FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
             T    +A E+ G++IP AF++ +   F K YG  K T+A  +N EF   L +M Y
Sbjct  62   ITALCMADEAAGRRIPFAFLEDIHGFRVKTYGRA-ALTSLAYGMNDEFSRVLSQQMDYYS  120

Query 123   DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
            + P    ++ +++S+V+ VM+ +NI +KVL+RG++++ +VDKT N++    F++Q
Sbjct 121   NDPN-ADRINRMRGEISQVRTVMIDNIDKVLERGDRLDMLVDKTANMQGNTIRFRQARR  179

Query 183   VRRKMWLQNMKIKLIVLGIIIALILILIILSVCHGF  217
             R   W +N+K+ + ++ ++ +I ++++ +CHGF
Sbjct 180   FRNTTWWRNVKLTIALIFLLTVIIYVVLVFMCHGF  214


>gb|ABK95432.1|  unknown [Populus trichocarpa]
Length=220

 Score = 145 bits (366),  Expect = 2e-33, Method: Compositional matrix adjust.
 Identities = 74/213 (34%), Positives = 135/213 (63%), Gaps = 3/213 (1%)

Query   5   SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNK-FTYNCDGHTFNYLVEDGF   63
            +++YA VARG+V+LAE++     N + IA Q L K+P +++   +Y+ D + F+   DG
Sbjct   2   AILYALVARGSVVLAEFSSTATNASAIARQILDKIPGNDDSNVSYSQDRYIFHVKRTDGL   61

Query  64   TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
             +AE+ G++IP AF++ + + F + YG   +N EF  L + M+Y +
Sbjct  62   AVLCMADETAGRRIPFAFLEDIHQFRARTYGRA-VITAQAYAMNDEFSRVLSQQMEYYTN  120

Query 124   HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
            P    ++ ++S+V+ VM+EN+ +KVL+RG++I++ +VDKT N++    F++Q
Sbjct 121   DPN-ADRINRLKGEMSQVRNVMIENIDKVLERGDRLELLVDKTANMQGNTFRFRKQARRF  179

Query 184   RRKMWLQNMKIKLIVLGIIIALILILLLSVCHG  216
            +W +N+K+ + ++ +++ +I +++  VCHG
Sbjct 180   SSAVMWWRNVKLTVALILLLLVIIYVVLAVVCHG  212


>ref|XP_001635801.1|  G predicted protein [Nematostella vectensis]
 gb|EDO43738.1|  G predicted protein [Nematostella vectensis]
```

```
    Length=218

      GENE ID: 5515684 NEMVEDRAFT_v1g183227 | predicted protein
    [Nematostella vectensis] (10 or fewer PubMed links)

      Score = 140 bits (354), Expect = 5e-32, Method: Compositional matrix adjust.
      Identities = 74/191 (38%), Positives = 111/191 (58%), Gaps = 3/191 (1%)

    Query  6    LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY  65
                L Y+ +ARG   IL +Y E TGNF  +  L K+P ++ K TY    + F+ +VEDG Y
    Sbjct  3    LYYSLIARGGTILVDYAETTGNFQQVTYTILEKIPGNDTKCTYVSGSYQFHVIVEDGLVY  62

    Query  66   CVVAVESVGQQIPIAFMDRVKEDFTKRYGGKAATAAANSLNREFGSKLKEHMQYCVDHP   125
                +A + G++ P AF++ +K  F+      +A TA +   R+F   L     M   D P
    Sbjct  63   LCMADKEFGKKDPYAFLEEIKRRFSNSSLKARARTAQSFEFKRDFAQVLATQMALYSD-P  121

    Query  126  EEVSKLA---KVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
                     A   KV+ +V EVK VM +NIEKVL+RGE+I++L+DK E L + AQ F++  + +
    Sbjct  122  GRAGGDAINKVQREVDEVKDVMTKNIEKVLERGERIDILMDKAETLDNSAQTFQRHSSRL  181

    Query  184  RRKMWLQNMKI  194
                R+KMW QN ++
    Sbjct  182  RKKMWWQNTRM  192


    >ref|NP_180106.1| [UG] ATVAMP712 (Arabidopsis thaliana vesicle-associated membran
    712)
     sp|Q9SIQ9|VA712_ARATH [G] Vesicle-associated membrane protein 712 (AtVAMP712)
     gb|AAD23657.1| [G] putative synaptobrevin [Arabidopsis thaliana]
    Length=219

      GENE ID: 817072 ATVAMP712 | ATVAMP712 (Arabidopsis thaliana vesicle-associated
    membrane protein 712) [Arabidopsis thaliana] (10 or fewer PubMed links)

      Score = 140 bits (354), Expect = 5e-32, Method: Compositional matrix adjust.
      Identities = 75/213 (35%), Positives = 133/213 (62%), Gaps = 3/213 (1%)

    Query  5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPAS-NNKFTYNCDGHTFNYLVEDGF  63
                S++YA VARGTV+LAE +   N +TIA Q L K+P + ++  +Y+ D + F+     DG
    Sbjct  2    SILYALVARGTVVLAELSTTSNASTIAKQILEKIPGNDSHVSYSQDRYVFHVKRTDGL  61

    Query  64   TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD  123
                T   +A E G++IP +F++ + + F  YG     +A +A++N EF    L + ++Y  +
    Sbjct  62   TVLCMADEDAGRRIPFSFLEDIHQRFVRTYGRA-IHSAQAYAMNDEFSRVLNQQIEYYSN  120

    Query  124  HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV  183
                 P   ++++K ++++V+ VM+ENI+ +LDRGE+LELLVDKT N++    FR+Q
    Sbjct  121  DPN-ADTISRIKGEMNQVRDVMIENIDNILDRGERLELLVDKTANMQGNTFRFRKQTRRF  179

    Query  184  RRKMWLQNMKIKLIVLGIIIALILIIILSVCHG  216
                +W +N K+ L+++ +++ +I I +   CHG
    Sbjct  180  NNTVWWRNCKLTLLLILVLLVIIYIGVAFACHG  212


    >ref|NP_001048427.1| [UG] Os02g0803600 [Oryza sativa (japonica cultivar-group)]
     dbj|BAD36041.1| [G] putative synaptobrevin 1 [Oryza sativa Japonica Group]
     dbj|BAF11341.1| [G] Os02g0803600 [Oryza sativa (japonica cultivar-group)]
    Length=226

      GENE ID: 4331049 Os02g0803600 | Os02g0803600 [Oryza sativa Japonica Group]
    (10 or fewer PubMed links)

      Score = 137 bits (346), Expect = 4e-31, Method: Compositional matrix adjust.
      Identities = 73/217 (33%), Positives = 127/217 (58%), Gaps = 9/217 (4%)

    Query  8    YAFVARGTVILAEYTEFT-GNFTTIASQCLMKLPASNN------YCYNCDGHTFNYLVE  60
                YA VARG V++AE+ +     N  +A Q L +A +        +Y  D H F+
    Sbjct  6    YAAVARGAVVMAEHGDAAFPNAGAVARQILDRLSAGDGGGGDCNISYTQDLHVFHVKRT  65

    Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGKAATAAANSLNREFGSKLKEHMQY  120
                DG T   +A ++ G++IP AF++ +    F K YG   A TA A ++N EF    L + M Y
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Sbjct   66   DGVTALCMADDAAGRRIPFAFLEDIHGRFVKTYGRA-ALTALAYAMNDEFSRVLGQQMDY   124

Query  121   CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG   180
             + P   +++++++ ++ +V+ VM++NI+KVL+RG+++ELLVDKT   ++    F++Q
Sbjct  125   YSNDPN-ADRISRMRGEMDQVRNVMIDNIDKVLERGDRLELLVDKTATMQGNTMRFKRQA   183

Query  181   TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF   217
             R   +W +N+K+     + I++ +I I+++ +CHGF
Sbjct  184   RRFRNTVWWRNVKLTAASVFILLVIIYIVLVYMCHGF   220


>ref|NP_001086871.1| U G  synaptobrevin-like 1 [Xenopus laevis]

 gb|AAH77586.1| G  Sybl1-prov protein [Xenopus laevis]
Length=220

 GENE ID: 446706 sybl1 | synaptobrevin-like 1 [Xenopus laevis]
(10 or fewer PubMed links)

 Score =  137 bits (345),  Expect = 5e-31, Method: Compositional matrix adjust.
 Identities = 71/192 (36%), Positives = 115/192 (59%), Gaps = 6/192 (3%)

Query    5   SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             ++++A VARGT ILA++   GNF +  Q L K+P+ NNK TY+  + F+Y+ +D
Sbjct    2   AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGSYLFHYMCQDRII   61

Query   65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH   124
             Y  +  + +   F++ +K+ F  YG +A TA   +F S L   ++Y H
Sbjct   62   YLCITDDDFERSRAFNFLNEIKKRFQTTYGS-RAQTALPYAMNSEFSSVLSAQLKY---H   117

Query  125   PE--EVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN   182
             E   V ++A+ +AQV E+KG+M+ NI+ V  RGE++ELL+DKTENL    F+    N
Sbjct  118   SENKSVDRVAETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKITSRN   177

Query  183   VRRKMWLQNMKI   194
             + R M  ++N+K+
Sbjct  178   LARAMCMKNLKL   189


>ref|XP_566592.1| G  vesicle-associated membrane protein 712 [Cryptococcus neofor
var. neoformans JEC21]

 gb|AAW40773.1| G  vesicle-associated membrane protein 712, putative [Cryptococcu
neoformans var. neoformans JEC21]
Length=306

 GENE ID: 3253707 CNA02090 | vesicle-associated membrane protein 712
[Cryptococcus neoformans var. neoformans JEC21] (10 or fewer PubMed links)

 Score =  136 bits (343),  Expect = 8e-31, Method: Compositional matrix adjust.
 Identities = 73/192 (38%), Positives = 116/192 (60%), Gaps = 5/192 (2%)

Query    5   SLIYAFVARGTVILAEYTEFTGNFTTIAS-QCLMKLPASNNKFTYNCDGHTFNYLVEDGF   63
             SLI+A +ARGT +LAE+    T     A   L K+P +N+K TY    +Y+   +G
Sbjct   89   SLIHALIARGTTVLAEHATGTAELKPAAQITILSKIPPNNSKLTYVWQDRLIHYVSSNGV   148

Query   64   TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHM-QYCV   122
             Y V+A +SVG+++P AF+  ++  FT +Y    +A+SL  EF +L + M  QY
Sbjct  149   IYLVMADDSVGRRMPFAFLADLERRFTAQYESDDIVSAGAHSLE-EFEPELAKLMHQYTS   207

Query  123   DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN   182
             P +  L + ++ +++ VK +M++NI+ +L RGE+++LLVDKT+ L  QA  FR+ +
Sbjct  208   SPPAD--PLRQAQSDLNNVKDIMVQNIDSILQRGERLDLLVDKTDTLAGQAYAFRRGARS   265

Query  183   VRRKMWLQNMKI   194
             VRR+ W +NM+I
Sbjct  266   VRRQQWWKNMRI   277


>ref|XP_778199.1| G  hypothetical protein CNBA1990 [Cryptococcus neoformans var.
B-3501A]

 gb|EAL23552.1| G  hypothetical protein CNBA1990 [Cryptococcus neoformans var. ne
B-3501A]
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Length=306

  GENE ID: 4933450 CNBA1990 | hypothetical protein
[Cryptococcus neoformans var. neoformans B-3501A]

  Score = 136 bits (342),  Expect = 1e-30, Method: Compositional matrix adjust.
  Identities = 73/192 (38%), Positives = 116/192 (60%), Gaps = 5/192 (2%)

Query  5    SLIYAFVARGTVILAEYTEFTGNFTTIAS-QCLMKLPASNNKFTYNCDGHTFNYLVEDGF  63
            SLI+A +ARGT +LAE+     T      A   L K+P +N+K TY      +Y+ +G
Sbjct  89   SLIHALIARGTTVLAEHATGTAELKPAAQITILSKIPPNNSKLTYVWQDRLIHYVSSNGV  148

Query  64   TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHM-QYCV  122
            Y V+A +SVG+++P AF+   ++   FT +Y      +A A+SL  EF  +L + M QY
Sbjct  149  IYLVMADDSVGRRMPFAFLADLERRFTAQYESDDIVSAGAHSLE-EFEPELAKLMHQYTS  207

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
               P +   L + ++ ++ VK +M++NI+ +L RGE+++LLVDKT+ L  QA  FR+ +
Sbjct  208  SPPAD--PLRQAQSDLNNVKDIMVQNIDSILQRGERLDLLVDKTDTLAGQAYAFRRGARS  265

Query  183  VRRKMWLQNMKI  194
            VRR+ W +NM+I
Sbjct  266  VRRQQWWKNMRI  277


>ref|NP_001026292.1| [UG] synaptobrevin-like 1 [Gallus gallus]
  sp|Q5ZL74.1|VAMP7_CHICK [G] Vesicle-associated membrane protein 7 (Synaptobrevin-
1)
  emb|CAG31519.1| [G] hypothetical protein [Gallus gallus]
Length=220

  GENE ID: 422297 RCJMB04_7f19 | vesicle-associated membrane protein 7
[Gallus gallus] (10 or fewer PubMed links)

  Score = 135 bits (341),  Expect = 1e-30, Method: Compositional matrix adjust.
  Identities = 71/192 (36%), Positives = 114/192 (59%), Gaps = 6/192 (3%)

Query  5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
            ++++A VARGT ILA++    GNF  +  Q L K+P+ NNK TY+   + F+Y+ +D
Sbjct  2    AILFAVVARGTTILAKHAWCGGNFLEVTEGILAKIPSENNKLTYSHGNYLFHYICQDRII  61

Query  65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            Y  +   +    F++ +K+ F  YG  +A  +N EF S L    +Y   H
Sbjct  62   YLCITDDDFERSRAFNFLNEIKKRFQTYGS-RAQTALPYAMNSEFSSVLAAQLKY---H  117

Query  125  PEE--VSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
             E      ++A+ +AQV E+KG+M+ NI+ V  RGEK+ELL+DKTENL    F+     N
Sbjct  118  SESKGTDQVAETQAQVDELKGIMVRNIDLVAQRGEKLELLIDKTENLVDSSVTFKTTSRN  177

Query  183  VRRKMWLQNMKI  194
            + R M ++N+K+
Sbjct  178  LARAMCMKNLKL  189


>gb|ABP03854.1| Longin-like [Medicago truncatula]
Length=224

  Score = 135 bits (340),  Expect = 2e-30, Method: Compositional matrix adjust.
  Identities = 70/217 (32%), Positives = 127/217 (58%), Gaps = 9/217 (4%)

Query  6    LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKF-----TYNCDGHTFNYLVE  60
            ++Y  VARG V+LAE++    N + A Q L ++     N +    +++ D + F+
Sbjct  3    ILYGMVARGQVVLAEFSVIQSNASVVAKQILNQINQGTNSYNDSNVSFSHDRYVFHVRRT  62

Query  61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY  120
            DG T  +A E+ G++IP +F++ +   +    F KY G  +A A ++N EF   L + M Y
Sbjct  63   DGLTVLCMADEAFGRRIPFSFLEDIHNRFVKTYAGA-ILSAPAYTMNDEFSRILSQQMDY  121

Query  121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG  180
              P  +L ++K ++++V+ VM+ NI+KVL+RG +E+LV+KT + +   F++Q
Sbjct  122  YSTDPN-ADRLNRLKGEMTQVRTVMLDNIEKVLERGGRLEMLVEKTATMNTNSVRFKRQA  180

Query  181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILS-VCHG  216
```

```
                + MW  N+++  + L +I A++  IIL+ +CHG
Sbjct 181   RRYKNNMWWSNVRLT-VALIMIFAIVFYIILAFMCHG  216
```

>ref|NP_610524.1| **UG** CG1599 CG1599-PA [Drosophila melanogaster]
 gb|AAF58892.1| **G** CG1599-PA [Drosophila melanogaster]
 gb|AAL49317.1| **G** RH15778p [Drosophila melanogaster]
Length=218

 GENE ID: 36015 CG1599 | CG1599 [Drosophila melanogaster]
 (10 or fewer PubMed links)

 Score = 135 bits (339), Expect = 2e-30, Method: Compositional matrix adjust.
 Identities = 69/211 (32%), Positives = 124/211 (58%), Gaps = 3/211 (1%)

```
Query 6     LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY  65
            ++Y+ ++RGT +LA++ E  GNF  +   + ++  N+K TY    +Y E+   Y
Sbjct 3     ILYSVISRGTTVLAKFAECVGNFAEVTEHIIGRIGVHNHKMTYTHGDYLIHYTCENKLVY  62

Query 66    CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP  125
             +      +   +   F+  +K+ F + YG  + ATA A S+N EF    L + M Y
Sbjct 63    MCITDNEFERSRAFLFLADIKQKFIQTYGL-QVATAIAYSMNTEFSKILAQQMVY-FSQS  120

Query 126   EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR  185
             EV  +++V  Q+ E+K +M++NI+ + DRGEK+ELLV+KTENL + +  FR+   N+ R
Sbjct 121   REVDTISRVHGQIDELKDIMVKNIDSLRDRGEKLELLVNKTENLSNNSVAFRKASRNLAR  180

Query 186   KMWLQNMKIKLIVLGIIIALILIIILSVCHG  216
            +M+ +N+++  +V+G++I  I+ +I+S+  G
Sbjct 181   QMFWKNIRV-YVVVGLVITFIVYVIVSMACG  210
```

>ref|NP_035645.1| **UG** vesicle-associated membrane protein 7 [Mus musculus]
 sp|P70280.1|VAMP7_MOUSE **G** Vesicle-associated membrane protein 7 (VAMP-7) (Synap
protein 1)
 emb|CAA65509.1| **G** synaptobrevin-like protein [Mus musculus]
 8 more sequence titles

 emb|CAB94231.1| **G** synaptobrevin-like protein [Mus musculus]
 dbj|BAB22386.1| **G** unnamed protein product [Mus musculus]
 dbj|BAB27667.1| **G** unnamed protein product [Mus musculus]
 gb|AAH03764.1| **G** synaptobrevin like 1 [Mus musculus]
 dbj|BAC40712.1| **G** unnamed protein product [Mus musculus]
 dbj|BAE38126.1| **G** unnamed protein product [Mus musculus]
 gb|ABK42476.1| VAMP7 [synthetic construct]
 gb|EDL07809.1| **G** synaptobrevin like 1, isoform CRA_c [Mus musculus]
Length=220

 GENE ID: 20955 Vamp7 | vesicle-associated membrane protein 7 [Mus musculus]
 (Over 10 PubMed links)

 Score = 134 bits (337), Expect = 4e-30, Method: Compositional matrix adjust.
 Identities = 71/192 (36%), Positives = 115/192 (59%), Gaps = 6/192 (3%)

```
Query 5     SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
            ++++A VARGT ILA++   GNF  +  Q L K+P+ NNK TY+   + F+Y+ +D
Sbjct 2     AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV  61

Query 65    YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
            Y  + +   +   +F++ VK+ F  YG +A TA   ++N EF S L    +++    H
Sbjct 62    YLCITDDDFERSRAFSFLNEVKKRFQTTYGS-RAQTALPYAMNSEFSSVLAAQLKH---H  117

Query 125   PEEVS--KLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
             E S   K+ +  +AQV E+KG+M+ NI+ V  RGE++ELL+DKTENL   + F+   N
Sbjct 118   SENKSLDKVMETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN  177

Query 183   VRRKMWLQNMKI  194
```

```
               + R M ++N+K+
Sbjct  178   LARAMCMKNIKL   189


>emb|CAH69613.1|  synaptobrevin 1-2 [Paramecium tetraurelia]
Length=228

 Score =  134 bits (337),  Expect = 4e-30, Method: Compositional matrix adjust.
 Identities = 71/216 (32%), Positives = 130/216 (60%), Gaps = 3/216 (1%)

Query  6     LIYAFVARGT-VILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
             +IYA V RG+ V+L+EY+   GN+   A   K+  SN K ++N + + F+ LVEDGF
Sbjct  8     IIYAVVVRGSNVVLSEYSIAKGNYIAFAKTIISKVNQSNAKKSFNYEQYEFHILVEDGFS  67

Query  65    YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
             + ++A   +I A ++ +K+ F + +   + A + LN +F + K  +Y   +
Sbjct  68    FLIMAERGLKMRIAFACLEDMKQKFFQMFQPQQRDQAISYGLNSQFSIEQKNKIEYY--N  125

Query  125   PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
                 + KL  V   + + K VMMEN++K+L+RGEKI++LV+KT   + +    ++ T +R
Sbjct  126   SPQADKLRMVSDNIQQTKEVMMENLDKLLERGEKIDILVEKTNVMVNISTSMKENATTLR  185

Query  185   RKMWLQNMKIKLIVLGIIIALILIIILSVCHGPKCH   220
             R+MW +N+K+ +I++ + +  I I++  C GF  H
Sbjct  186   RQMWWRNIKMTIILVLVGLLAIYIIMVIACGGFAMH   221


>ref|XP_001439963.1| [G] hypothetical protein GSPATT00008957001 [Paramecium tetrau
strain d4-2]
 emb|CAD97455.1|  synaptobrevin 1 [Paramecium tetraurelia]
 emb|CAK72566.1| [G] unnamed protein product [Paramecium tetraurelia]
Length=228

 GENE ID: 5025748 GSPATT00008957001 | hypothetical protein
[Paramecium tetraurelia strain d4-2]

 Score =  134 bits (337),  Expect = 4e-30, Method: Compositional matrix adjust.
 Identities = 72/216 (33%), Positives = 125/216 (57%), Gaps = 3/216 (1%)

Query  6     LIYAFVARGT-VILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
             +IYA VARG+ V+L+EY+   GN+   + L K+  N K ++N + + F+ LVEDGF
Sbjct  8     IIYAVVARGSNLFLSEYSILKGNYIDFSKTILSKVNQQNAKKSFNYEQYEFHILVEDGFS  67

Query  65    YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
             + ++A   +I A ++ +K+ F + +   + A + LN +F + K  +QY
Sbjct  68    FLIMADRGLKMRIAFACLEDMKQKFFQMFTPQQRDKAMSYGLNSQFSIEQKNQIQYY--N  125

Query  125   PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
                 + KL  V   + + K VMMEN++K+L+RG+KIE+LV KT+   +     R  T +R
Sbjct  126   SPQADKLRMVSDNIQQTKDVMMENLDKLLERGDKIEILVVKTDQMAMLSTTMRTNATTLR  185

Query  185   RKMWLQNMKIKLIVLGIIIALILIIILSVCHGPKCH   220
             R+MW +N K+ LI++ + +   I  I++  C GF  H
Sbjct  186   RQMWWRNKKMMLIMILVGLLAIYFIMVIACGGFAMH   221


>ref|XP_795809.2| [U][G] PREDICTED: similar to Sybl1-prov protein [Strongylocentrot
purpuratus]
 ref|XP_001188931.1| [G] PREDICTED: similar to Sybl1-prov protein [Strongylocentro
purpuratus]
Length=220

 GENE ID: 591136 LOC591136 | similar to Sybl1-prov protein
[Strongylocentrotus purpuratus]

 Score =  134 bits (336),  Expect = 5e-30, Method: Compositional matrix adjust.
 Identities = 68/212 (32%), Positives = 125/212 (58%), Gaps = 1/212 (0%)

Query  6     LIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY  65
             ++YA +ARGT +LA Y   GNFT +  Q LMK+P  N K LTYSHGAYLFHYVSDERIIY
Sbjct  3     ILYAVIARGTTVLANYAACQGNFTEVTEQVLMKIPPQNAKLTYSHGAYLFHYVSDERIIY  62

Query  66    CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP  125
```

```
              +  +       AF+ +K+ FT  YG  + TA  ++N EF   L   ++Y
Sbjct  63     MCITDDDFERSRAFAFLQEIKKKFTATYGS-RVHTALPFAMNSEFSRVLAAQIRYFAQPL  121

Query  126    EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR  185
              +  +++++V+  + E+  +M+ NIE V +RGE++ELL+DKTE+L + +   F++   ++ R
Sbjct  122    SDHTRMSEVQQDLEELNQIMVRNIESVSNRGERLELLIDKTEDLETTSLTFKKSSKSLAR  181

Query  186    KMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
              M+++N+K+  +I+  ++I  +I   I+ + C G
Sbjct  182    SMFMKNLKLIIILSIVVILVIYFIVSAACGGL  213
```

>dbj|BAD96514.1| 🅖 synaptobrevin-like 1 variant [Homo sapiens]
Length=220

 GENE ID: 6845 VAMP7 | vesicle-associated membrane protein 7 [Homo sapiens]
(Over 10 PubMed links)

 Score = 134 bits (336), Expect = 6e-30, Method: Compositional matrix adjust.
 Identities = 77/215 (35%), Positives = 128/215 (59%), Gaps = 6/215 (2%)

```
Query  5      SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
              ++++A VARGT ILA++   GNF +  Q L K+P+ NNK TY+  + F+Y+ +D
Sbjct  2      AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV  61

Query  65     YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
              Y  +  +      F++ +K+ F  YG +A TA  ++N EF S L   +++   H
Sbjct  62     YLCITDDDFERSRAFNFLNEIKKRFQTTYGS-RAQTAPPYAMNSEFSSVLAAQLKH---H  117

Query  125    PEE--VSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
              E   + K+ + +AQV E+KG+M+ NI+ V  RGE++ELL+DKTENL     +   F+    N
Sbjct  118    SENKGLDKVMETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN  177

Query  183    VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
              + R M+N ++N+K+ +I++ + I  I I++  +C GF
Sbjct  178    LARAMCMKNLKLTIIIIVSIVFIYIIVSPLCGGF  212
```

>ref|NP_005629.1| 🅄🅖 vesicle-associated membrane protein 7 [Homo sapiens]
  ref|XP_001100334.1| 🅄🅖 PREDICTED: synaptobrevin-like 1 isoform 3 [Macaca mulat
  ref|XP_001498248.1| 🅄🅖 PREDICTED: similar to ORF isoform 1 [Equus caballus]
  6 more sequence titles

sp|P51809.3|VAMP7_HUMAN 🅖 Vesicle-associated membrane protein 7 (VAMP-7) (Synapt
protein 1) (Tetanus-insensitive VAMP) (Ti-VAMP)
  emb|CAA63133.1| 🅖 ORF [Homo sapiens]
  emb|CAB96816.1| 🅖 synaptobrevin-like 1 protein [Homo sapiens]
  gb|AAH56141.1| 🅖 Vesicle-associated membrane protein 7 [Homo sapiens]
  gb|EAW55882.1| 🅖 synaptobrevin-like 1, isoform CRA_e [Homo sapiens]
  gb|EAW55883.1| 🅖 synaptobrevin-like 1, isoform CRA_e [Homo sapiens]
Length=220

 GENE ID: 6845 VAMP7 | vesicle-associated membrane protein 7 [Homo sapiens]
(Over 10 PubMed links)

 Score = 133 bits (335), Expect = 8e-30, Method: Compositional matrix adjust.
 Identities = 77/215 (35%), Positives = 128/215 (59%), Gaps = 6/215 (2%)

```
Query  5      SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT  64
              ++++A VARGT ILA++   GNF  +  Q L K+P+ NNK TY+   + F+Y+ +D
Sbjct  2      AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV  61

Query  65     YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
              Y  +  +      F++ +K+ F   YG +A TA  ++N EF S L   +++   H
Sbjct  62     YLCITDDDFERSRAFNFLNEIKKRFQTTYGS-RAQTALPYAMNSEFSSVLAAQLKH---H  117

Query  125    PEE--VSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
              E   + K+ + +AQV E+KG+M+ NI+ V  RGE++ELL+DKTENL     + F+    N
Sbjct  118    SENKGLDKVMETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN  177
```

```
Query  183   VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF   217
             + R M ++N+K+ +I++ + I   I II+  +C GF
Sbjct  178   LARAMCMKNLKLTIIIIIVSIVFIYIIVSPLCGGF   212
```

>ref|XP_855489.1| **UG** PREDICTED: similar to Synaptobrevin-like protein 1 [Canis
Length=331

 GENE ID: 612663 VAMP7 | vesicle-associated membrane protein 7
[Canis lupus familiaris]

 Score = 133 bits (334), Expect = 9e-30, Method: Compositional matrix adjust.
 Identities = 75/213 (35%), Positives = 129/213 (60%), Gaps = 2/213 (0%)

```
Query    5   SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             ++++A VARGT ILA++    GNF  + Q L K+P+ NNK TY+  + F+Y+ +D
Sbjct  113   AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV  172

Query   65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
             Y + +   +    F++ +K+ F    YG  +A TA    ++N EF S L   +++  ++
Sbjct  173   YLCITDDDFERSRAFNFLNEIKKRFQTTYGS-RAQTALPYAMNSEFSSVLAAQLKHHSEN  231

Query  125   PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
             + + K+ + +AQV E+KG+M+ NI+ V  RGE++ELL+DKTENL     + +     N+
Sbjct  232   -KGIDKVVETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRNLA  290

Query  185   RKMWLQNMKIKLIVLGIIIALILIIILSVCHGF · 217
             R M ++N+K+ +I++ + I   I II+  +C GF
Sbjct  291   RAMCMKNLKLTIIIIIVSIVFIYIIVSPLCGGF  323
```

>ref|XP_001459953.1| **UG** hypothetical protein GSPATT00025290001 [Paramecium tetr
strain d4-2]
 emb|CAK92556.1| **G** unnamed protein product [Paramecium tetraurelia]
Length=228

 GENE ID: 5045738 GSPATT00025290001 | hypothetical protein
[Paramecium tetraurelia strain d4-2]

 Score = 133 bits (334), Expect = 9e-30, Method: Compositional matrix adjust.
 Identities = 71/216 (32%), Positives = 129/216 (59%), Gaps = 3/216 (1%)

```
Query    6   LIYAFVARGT-VILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             +IYA V RG+ V+L+EY+    GN+   A   + SN K ++N   A   S++ ++DGF
Sbjct    8   IIYAVVVRGSNVVLSEYSIAKGNYIAFAKTIISKVNQSNAKKSFNYEQYEPHILVEDGFS   67

Query   65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
             + ++A  +  +I A ++ +K+ F + +   A + LN +F + K  ++Y  +
Sbjct   68   FLIMAERGLKMRIAFACLEDMKQKFFQMFQPQQRDQAISYGLNSQFSIEQKNKIEYY--N  125

Query  125   PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
             + KL  V  + K VMMEN++K+L+RGEKI++LV+KT   + +   ++ T +R
Sbjct  126   SPQADKLRMVSDNIQQTKEVMMENLDKLLERGEKIDILVEKTNVMVNISTSMKENATTLR  185

Query  185   RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH   220
             R+MW +N K+ +I++ + +   I II++  C GF  H
Sbjct  186   RQMWWRNKKMTIILVLVGLLAIYIIMVIACGGFAMH  221
```

>ref|NP_445983.1| **UG** vesicle-associated membrane protein 7 [Rattus norvegicus]
 sp|Q9JHW5.1|VAMP7_RAT **G** Vesicle-associated membrane protein 7 (VAMP-7) (Synapto
protein 1)
 gb|AAF88059.1|AF281632_1 **G** vesicle-associated membrane protein 7 [Rattus norveg
 gb|EDL83883.1| **G** synaptobrevin-like 1, isoform CRA_b [Rattus norvegicus]
Length=220

 GENE ID: 85491 Sybl1 | synaptobrevin-like 1 [Rattus norvegicus]
(10 or fewer PubMed links)

 Score = 133 bits (334), Expect = 9e-30, Method: Compositional matrix adjust.

```
         Identities = 75/213 (35%), Positives = 128/213 (60%), Gaps = 2/213 (0%)

Query   5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             ++++A VARGT ILA++     GNF   + Q L K+P+ NNK TY+   + F+Y+ +D
Sbjct   2    AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV   61

Query   65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
             Y +  +  +    F++ VK+ F   YG  +A TA   ++N EF S L  +++ ++
Sbjct   62   YLCITDDDFERSRAFGFLNEVKKRFQTTYGS-RAQTALPYAMNSEFSSVLAAQLKHHSEN  120

Query   125  PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR  184
             + + ++ + +AQV E+KG+M+ NI+ V  RGE++ELL+DKTENL   F+    N+
Sbjct   121  -QSLDRVTETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRNLA  179

Query   185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
             R M ++N+K+  I++ + I  I II+  +C GF
Sbjct   180  RAMCVKNVKLTAIIVVVSIVFIYIIVSPLCGGF  212


>ref|NP_001069770.1| U G vesicle-associated membrane protein 7 [Bos taurus]
  sp|Q17QI5.1|VAMP7_BOVIN G Vesicle-associated membrane protein 7 (VAMP-7) (Synap
tobrevin 1)
  gb|AAI18342.1| G Similar to Synaptobrevin-like protein 1 [Bos taurus]
Length=220

 GENE ID: 613984 SYBL1 | vesicle-associated membrane protein 7 [Bos taurus]

 Score =  133 bits (334),  Expect = 9e-30, Method: Compositional matrix adjust.
 Identities = 77/215 (35%), Positives = 128/215 (59%), Gaps = 6/215 (2%)

Query   5    SLIYAFVARGTVILAEYTEFTGNFTTIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT   64
             ++++A VARGT ILA++     GNF   + Q L K+P+ NNK TY+   + F+Y+ +D
Sbjct   2    AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV   61

Query   65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH  124
             Y +  +  +     F++ +K+ F   YG  +A TA   ++N EF S L  +++  H
Sbjct   62   YLCITDDDFERSRAFNFLNEIKKRFQTTYGS-RAQTALPYAMNSEFSSVLAAQLKH---H  117

Query   125  PEE--VSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN  182
             E   + K++ +AQV E+KG+M+ NI+ V  RGE++ELL+DKTENL   F+   N
Sbjct   118  SENKGLDKVMETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN  177

Query   183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF  217
             + R M ++N+K+  I++ I +  I II+  +C GF
Sbjct   178  LARAMCMKNLKLTIIIIIISVVFIYIIVSPLCGGF  212


>dbj|BAE99604.1| synaptobrevin-like protein [Arabidopsis thaliana]
Length=186

 Score =  133 bits (334),  Expect = 1e-29, Method: Compositional matrix adjust.
 Identities = 62/175 (35%), Positives = 112/175 (64%), Gaps = 2/175 (1%)

Query   42   SNNKFTYNCDGHTFNYLVEDGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATA  101
             S+ +  ++ D + F+ L  DG T+  +A ++ G+++ ++++ F  K YG   A A
Sbjct   6    SDERLCFSQDRYIFHILRSDGLTFLCMANDTFGRRVPFSYLEEIHMRFMKNYGK-VAHNA   64

Query   102  AANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIEL  161
             A ++N EF  L + M++   +P V  L +V++ +VSE++ +M+ENIEK+++RG++IEL
Sbjct   65   PAYAMNDEFSRVLHQQMEFFSSNPS-VDTLNRVRGEVSEIRSVMVENIEKIMERGDRIEL  123

Query   162  LVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF  216
             LVDKT  ++ +  FR+Q  +RR +W++N K+ +++  +I+ L+ III S C G
Sbjct   124  LVDKTATMQDSSFHFRKQSKRLRRALWMKNAKLLVLLTCLIVFLLYIIIASFCGG  178
```

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